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<b>(21) International Application Number:</b> PCT/GB98/01297 <b>(22) International Filing Date:</b> 5 May 1998 (05.05.98)  <b>(30) Priority Data:</b> 9710370.9                      20 May 1997 (20.05.97)                      GB  <b>(71) Applicant (for all designated States except US):</b> ZENECA LIMITED [GB/GB]; 15 Stanhope Gate, London W1Y 6LN (GB).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> BIRD, Colin, Roger [GB/GB]; Jealott's Hill Research Station, Bracknell, Berkshire RG42 6ET (GB). MEDINA-SUAREZ, Rosybel de Jesus [ES/GB]; 42 Thorndon Court, Eagle Way, Brentwood, Essex CM13 3BY (GB). SEYMOUR, Graham, Barron [GB/GB]; Horticulture Research International, Wellsbourne, Warwick CV35 9EF (GB).  <b>(74) Agents:</b> HUSKISSON, Frank, Mackie et al.; Zeneca Agrochemicals, Intellectual Property Dept., Jealott's Hill Research Station, P.O. Box 3538, Bracknell, Berkshire RG42 6YA (GB).			<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
<b>(54) Title:</b> GENETIC CONTROL OF FRUIT RIPENING  <b>(57) Abstract</b>  A method of modulating the ripening and/or senescence characteristics in plants of the genus <i>Musa</i> comprises transforming plants with one or more sequences obtainable from the deposited cDNA library having the accession number 40183, regenerating said plants and selecting from the population of transformants those plants having modulated and/or tissue senescence characteristics.			

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## GENETIC CONTROL OF FRUIT RIPENING

This invention relates generally to the modification of a plant phenotype by the regulation of plant gene expression. More specifically it relates to the modulation of the ripening and/or tissue senescence characteristics and plants derived therefrom.

Two principal methods for the control of expression are known, viz.: overexpression and underexpression. Overexpression is achieved by insertion of one or more than one extra copies of the selected gene. It is, however, not unknown for plants or their progeny, originally transformed with one or more than one extra copy of a nucleotide sequence, to exhibit the effects of underexpression as well as overexpression.

For underexpression there are two principle methods which are commonly referred to in the art as "antisense downregulation" and "sense downregulation, "cosuppression" or "gene silencing". Both of these methods lead to an inhibition of expression of the target gene. Other lesser used methods involve modification of the genetic control elements, the promoter and control sequences, to achieve greater or lesser expression of an inserted gene.

There is no reason to doubt the operability of sense/cosuppression technology. It is well established, used routinely in laboratories around the world and products in which it is used are on the market.

Gene control by any of these methods requires the insertion of the most favoured gene or genes into plant material which can be regenerated into plants. This transformation process can be performed via a number of methods, for example: the agrobacterium-mediated transformation method.

In the microparticle bombardment method, microparticles of dense material, usually gold or tungsten, are fired at high velocity at the target cells where they penetrate the cells, opening an aperture in the cell wall through which DNA may enter. The DNA may be coated on to the microparticles or may be added to the culture medium.

In microinjection, the DNA is inserted by injection into individual cells via an ultrafine hollow needle.

Another method, viz. fibre-mediated transformation, applicable to both monocots and dicots, involves creating a suspension of the target cells in a liquid, adding microscopic needle-like material, such as silicon carbide or silicon nitride "whiskers",

and agitating so that the cells and whiskers collide and DNA present in the liquid enters the cell.

In summary then, the requirements for both sense and antisense technology are known and the methods by which the required sequences may be introduced are known.

- 5 What remains then is to identify genes whose regulation will be expected to have a desired effect, isolate them or isolate a fragment of sufficiently effective length, construct a chimeric gene in which the effective fragment is inserted between promoter and termination signals, and insert the construct into cells of the target plant species by transformation. Whole plants may then be regenerated from the
- 10 transformed cells.

One suitable application of the present invention is the modulation of ripening and/or senescence processes in banana.

- Bananas are a globally important fruit crop. They are not only a popular dessert fruit, but represent a vital carbohydrate staple in the tropics with as many as 100 million
- 15 people subsisting on bananas and plantains as their main energy source. The cultivated dessert banana is commonly triploid, parthenocarpic and belongs to the musa AAA genome group, eg. Cavendish subtypes. Bananas are climacteric fruits and ripening is regulated by ethylene produced by the fruit and involves numerous biochemical changes including the conversion of starch to sugars, cell wall disassembly, synthesis
- 20 of volatile compounds, changes in phenolic constituents and degradation of chlorophyll in the peel. The conversion of starch to sugars is particularly striking, where starch accounts for 20-25% of the fresh weight of the unripe fruit and depending on the genetic background, can be converted almost entirely to sugars.
- The triploid nature of the cultivated dessert banana crop has hampered conventional
- 25 methods of breeding for improved characteristics. As a result of this an enormous pool of genetic resources for enhancing postharvest characteristics of the fruit has remained untapped.

- According to the present invention there is provided a method of modulating the fruit ripening or tissue senescence characteristics of a plant of the genus *Musa* comprising
- 30 inserting into the genome of said plant a DNA construct comprising in sequence a promoter region which is operable in plant cells, a DNA having a nucleotide sequence selected from SEQ ID Nos. 1-73, complementary sequences of SEQ ID Nos. 1-73 and

variants of said sequences permitted by degeneracy of the genetic code and a transcription termination sequence, and selecting from the population of regenerants those transformants with modulated fruit ripening or tissue senescence characteristics.

- 5 The invention also provides a method as described above wherein the said DNA insert comprises a full length polynucleotide coding sequence which includes a polynucleotide sequence as shown in any one of SEQ ID Nos. 1-73.
- The promoter of the said DNA construct may be constitutive, developmentally regulated, or switchable. It may additionally be tissue specific or organ specific.
- 10 The promoter may specifically be either the SAG 1 promoter, the polyubiquitin promoter or the banana ACC oxidase promoter.
- Suitable transformation methods for use with the present invention include the *Agrobacterium*, microparticle bombardment, fibre mediated or direct insertion methods.
- 15 The invention further provides plant material, plants, their progeny and seed produced according to a method as described above characterised in that said plant material and plants exhibit modulated ripening or tissue senescence characteristics.

- The gene sequences of the present invention may be synthesised *ab initio*, using the
- 20 sequence data provided in the sequence listing provided herewith, or isolated from a library using the standard techniques known within the art. To assist the isolation of these polynucleotides we have deposited with the National Collection of Industrial & Marine Bacteria, St. Machar Drive, Aberdeen, UK, a cDNA library of the banana peel ripening related genes. The library was deposited on 9th July 1996 and has the
- 25 Accession Number 40813.

- Thus, this invention is based on the identification of genes which encode proteins involved in banana ripening-related processes, specifically within banana peel. The DNA sequences may be used in the process of modifying the plant ripening characteristics of plants and/or fruit.
- 30 By virtue of this invention banana plants can be generated which, amongst other phenotypic modifications, may have one or more of the following fruit characteristics: improved resistance to damage during harvest, packaging and transportation due to

slowing of the ripening and over-ripening processes; longer shelf life and better storage characteristics due to reduced activity of degradative pathways (e.g. cell wall hydrolysis); improved processing characteristics due to changed activity of proteins/enzymes contributing to factors such as: viscosity, solids, pH, elasticity;

5 improved flavour and aroma at the point of sale due to modification of the sugar/acid balance and other flavour and aroma components responsible for characteristics of the ripe fruit; modified colour due to changes in activity of enzymes involved in the pathways of pigment biosynthesis (e.g. lycopene,  $\beta$ -carotene, chalcones and anthocyanins); increased resistance to post-harvest pathogens such as fungi.

10 The activity of the ripening-related proteins may be either increased or reduced depending on the characteristics desired for the modified plant part (fruit, leaf, flower, etc). The levels of protein may be increased; for example, by incorporation of additional genes. The additional genes may be designed to give either the same or different spatial and temporal patterns of expression in the fruit. "Antisense" or  
15 "partial sense" or other techniques may be used to reduce the expression of ripening-related protein.

The activity of each ripening-related protein or enzyme may be modified either individually or in combination with modification of the activity of one or more other ripening-related proteins/enzymes. In addition, the activities of the ripening-related  
20 proteins/enzymes may be modified in combination with modification of the activity of other enzymes involved in fruit ripening or related processes.

DNA constructs according to the invention may comprise a base sequence at least 10 bases (preferably at least 35 bases) in length for transcription into RNA. There is no theoretical upper limit to the base sequence - it may be as long as the relevant mRNA  
25 produced by the cell - but for convenience it will generally be found suitable to use sequences between 100 and 1000 bases in length. The preparation of such constructs is described in more detail below.

As a source of the DNA base sequence for transcription, a suitable cDNA or genomic DNA or synthetic polynucleotide may be used. The isolation of suitable ripening-  
30 related sequences is described above; it is convenient to use DNA sequences derived from the ripening-related clones deposited at NCIMB in Aberdeen. Sequences coding for the whole, or substantially the whole, of the appropriate ripening-related protein

may thus be obtained. Suitable lengths of this DNA sequence may be cut out for use by means of restriction enzymes. When using genomic DNA as the source of a base sequence for transcription it is possible to use either intron or exon regions or a combination of both.

- 5 To obtain constructs suitable for expression of the appropriate ripening-related sequence in plant cells, the cDNA sequence as found in one of the banana plasmids or the gene sequence as found in the chromosome of the banana plant may be used. Recombinant DNA constructs may be made using standard techniques.

- In this specification "modulation" means either an increase or decrease. More specifically "modulation the ripening or tissue senescence process in plants" means an alteration being either an increase or decrease in the said processes relative to an untreated or transformed plant.

"Ripening process of plants" means the process of maturing or developing.

- 15 "Senescence" means the progressive deterioration in function of cells, tissues, organs etc., related to the period of time since that function commenced.

"Plant material" includes plant cells and any other type of plant regenerable material.

"Full length polynucleotide coding sequence" includes a polynucleotide coding for the whole or substantially the whole of the appropriate ripening related mRNA/protein.

The invention will now be described by way of an example where:

- 20 TABLE 1. Is a list of all the clones isolated from banana peel and the corresponding sequence identity number as provided in the sequence listing herein. The table also illustrates the approximate clone size, the percentage identity and nucleotide similarity based on the results obtained from comparisons with the EMBL sequence database. Therefore, the table provides the putative gene identity based on these comparisons, corresponding published sequences and their database accession numbers.

25 FIGURE 1. Plant transformation vector pUN, containing the UBI polyubiquitin promoter.

FIGURE 2. Plant transformation vector pSHYN, containing hygromycin resistance gene for selection of transformed plants.

- 30 FIGURE 3. Plant transformation vector pFAN, containing the banana ACC oxidase promoter.

## EXAMPLE 1

## Construction of a cDNA library of ripening genes

## 1.1 Isolation of messenger RNA

Total RNA was isolated from ripening (24 hours after ethylene treatment) banana peel  
5 (*Musa acuminata* cv. Grand Nain) as described by Chang et al, Plant Molecular  
Biology Reporter, Vol. 11(2) 113-116 (1993). Messenger RNA was isolated from  
total RNA by Oligo(dT)-cellulose chromatography according to Bantle et al.,  
Analytical Biochemistry 72, 413-427 (1976).

## 10 1.2 Synthesis of cDNA and Cloning into Vector

The first and second strands of the cDNAs were synthesised from the messenger  
RNAs using a commercial cDNA synthesis kit (Catalog No. 200450, ZAP Express™  
Gold Cloning kit, Stratagene Ltd, Cambridge, Cambs, UK). Double stranded cDNAs  
were cloned into the ZAP Express™ vector, packaged, mixed with plating bacteria to  
15 determine titre and for library screening, following instructions of the suppliers  
protocol.

## 1.3 Screening of the cDNA library from banana peel.

The unamplified cDNA library from ripening banana peel was differentially screened  
20 using cDNA from unripe and ripening banana peel tissue. A proportion of the library  
was plated individually at low density and duplicate plaque lifts made onto Hybond N  
nylon filters (Amersham) according to the manufacturer's instructions. One filter was  
hybridised to dCTP radiolabeled cDNA from green fruit and the duplicate filter  
hybridised to dCTP radiolabeled cDNA from ripening fruit. Hybridisations were at  
25 high stringency. Plaques hybridising preferentially with ripening or green radiolabeled  
cDNA were picked and replated for a second round of selection by differential  
screening. These clones were numbered as ripening up- or down-regulated peel  
clones. The clones were in-vivo excised from the ZAP express™ vector into the pBK-  
CMV phagemid vector using the ExAssist™ interference-resistant helper phage,  
30 following instructions from manufacturers protocol.



1.4 Characterisation of the ripening peel cDNA library and the ripening-related clones.

The ripening cDNA library from peel tissue were prepared with an efficiency of  $3.2 \times 10^5$  plaque-forming units per microgram of cDNA. The sizes of the inserts in the peel library was 0.4 - 6.7 Kb with a mean size insert of 1.47 Kb.

From the 250 plaques used in the first screen, 73 putative ripening-related clones were obtained. These 73 clones were partially sequenced using the ABI PRISMTM Dye Terminator Cycle Sequencing Ready Reaction kit with AmpliTaq® DNA polymerase (Applied Biosystems, Warrington, Cheshire, UK) with forward primers specific for the pBK-CMV vector. From these, the following ripening-related clones were selected. Comparisons of this sequences in the EMBL database using GCG ('Wisconsin') software has identified homologies for the clones listed in TABLE 1 below.

## EXAMPLE 2

Construction of partial sense RNA vectors with the maize polyubiquitin promoter. A vector is constructed using the sequences corresponding to a fragment of the inserts of one of the sequences 1 to 73. This fragment is synthesised by polymerase chain reaction using synthetic primers incorporating BamHI restriction sites suitable for cloning between a maize UBI polyubiquitin promoter (Christensen et al, 1992, Plant Molecular Biology, 18:675-689) and a nopaline synthase 3'end termination sequences in the vector pUN (Fig. 1.).

The partial sense expression cassette is excised by digestion with AscI, the ends of the fragment are made flush with T4 polymerase and it is cloned into the vector pSHYN (Fig. 2.) which has been cut with KpnI and the ends made flush with Klenow polymerase. pSHYN contains hygromycin resistance gene for selection of transformed plants.

After synthesis of the vector, the structure and orientation of the sequences are confirmed by DNA sequence analysis.

## EXAMPLE 3

Construction of partial sense RNA vectors with a fruit enhanced promoter.

The 1386bp HindIII fragment containing the banana ACC oxidase promoter (PCT Application No. WO97/38106) is cloned the HindIII site of a multiple cloning vector to give the vector pFAN.

- 5 A vector is constructed using the sequences corresponding to a fragment of the inserts of one of the sequences 1 to 73. This fragment is synthesised by polymerase chain reaction using synthetic primers incorporating BamHI restriction sites suitable for cloning between a maize UBI polyubiquitin promoter (Christensen et al, 1992, Plant Molecular Biology, 18:675-689) and a nopaline synthase 3' end termination sequences in the vector pFAN (Figure 3.)
- 10 The truncated sense expression cassette is excised by digestion with AscI, the ends of the fragment are made flush with T4 polymerase and it is cloned into the vector pSHYN (Fig. 2.) which has been cut with KpnI and the ends made flush with Klenow polymerase. pSHYN contains hygromycin resistance gene for selection of transformed plants.
- 15 After synthesis of the vector, the structure and orientation of the sequences are confirmed by DNA sequence analysis.

#### EXAMPLE 4

- Construction of an over-expression vector with the maize polyubiquitin promoter.
- 20 The complete sequence of a ripening related cDNA containing a full open-reading frame is inserted into the vectors described in EXAMPLE 2.

#### EXAMPLE 5

- 25 Construction of an over-expression vector with a fruit enhanced promoter.
- The complete sequence of a ripening related cDNA containing a full open reading frame is inserted into the vectors described in EXAMPLE 3.

#### EXAMPLE 6

- 30 Generation of transformed *Musa* plants.

Transformed *Musa* plants containing the vectors are produced by the method described in Sagi et al. (1995) Biotechnology. Vol. 13 pp 481-485. Regenerated transformed plants are identified by their ability to grow on hygromycin and grown to maturity. Ripening fruit are analysed for a modulation in their ripening related or senescence characteristics.

Other suitable transformation methods for banana are described in Sagi et al. (1994) Plant Cell Reports. Vol. 13. pp 262-266. and May et al. (1995) Biotechnology. Vol. 13 pp 486-492.

TABLE 1

Sequence Identity	Group	Clone no.	Size Kb	Gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ-ID-NO-1	Peel Upregulated	7	0.6,0.4	Aminocyclopropane carboxylic oxidase	86.5	415	Musa acuminata X91076
SEQ-ID-NO-2	Peel Upregulated	13	0.7,0.5	Aminocyclopropane carboxylic oxidase	94.7	152	Musa acuminata X91076
SEQ-ID-NO-3	Peel Upregulated	23	0.8	Aminocyclopropane carboxylic oxidase	99.6	227	Musa acuminata X91076
SEQ-ID-NO-4	Peel Upregulated	105	0.7,0.5	Aminocyclopropane carboxylic oxidase	99.6	227	Musa acuminata X91076
SEQ -ID-NO-5	Peel Upregulated	8	1.9	Aconitase	76	815	Cucurbita melo X82840
SEQ -ID-NO-6	Peel Upregulated	11	1.7	Pectate Lyase II	64.6	579	Zea mays L20140
SEQ -ID-NO-7	Peel Upregulated	12	1.8	Pectate Lyase I	58	276	Nicotiana tabacum X61102
SEQ -ID-NO-8	Peel Upregulated	22	1.8	Pectate Lyase I	61.2	389	Lilium longiflorum L18911
SEQ -ID-NO-9	Peel Upregulated	31	1.7	Pectate Lyase II	64.7	546	Zea mays L20140

Sequence Identity	Group	Clone no.	Size Kb	Gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-10	Peel Upregulated	51	1.7	Pectate Lyase II	66.3	661	Zea mays L20140
SEQ -ID-NO-11	Peel Upregulated	52	1.9	Pectate Lyase I	59.8	361	Lilium longiflorum L18911
SEQ -ID-NO-12	Peel Upregulated	57	1.8	Pectate Lyase II	61.9	491	Zea mays L20140
SEQ -ID-NO-13	Peel Upregulated	59	1.5	Pectate Lyase II	64.6	582	Zea mays L20140
SEQ -ID-NO-14	Peel Upregulated	68	6.7	Pectate Lyase II	68.2	352	Zea mays L20140
SEQ -ID-NO-15	Peel Upregulated	69	1.5	Pectate Lyase II	64.3	649	Zea mays L20140
SEQ -ID-NO-16	Peel Upregulated	85	1.5	Pectate Lyase II	64.2	584	Zea mays L20140
SEQ -ID-NO-17	Peel Upregulated	101	1.5	Pectate Lyase II	65.1	578	Zea mays L20140
SEQ -ID-NO-18	Peel Upregulated	113	1.8	Pectate Lyase I	56.4	557	Lilium longiflorum L18911

Sequence Identity	Group	Clone no.	Size Kb	Gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-19	Peel Upregulated	114	1.7	Pectate Lyase I	59.2	419	Licopersicon esculentum X55193
SEQ -ID-NO-20	Peel Upregulated	130	1.6	Pectate Lyase II	65.3	588	Zea mays L20140
SEQ -ID-NO-21	Peel Upregulated	139	1.7	Pectate Lyase I	55.1	535	Lilium longiflorum L18911
SEQ -ID-NO-22	Peel Upregulated	16	1.1	Endochitinase	73.6	671	Oriza sativa X56063
SEQ -ID-NO-23	Peel Upregulated	19	1.1	Endochitinase	71.6	690	Oriza sativa X56063
SEQ -ID-NO-24	Peel Upregulated	48	1	Endochitinase	71.1	774	Oriza sativa D16221
SEQ -ID-NO-25	Peel Upregulated	54	1.1	Endochitinase	69.7	634	Oriza sativa D16221
SEQ -ID-NO-26	Peel Upregulated	91	1.2	Endochitinase	68.1	740	Oriza sativa D16221
SEQ -ID-NO-27	Peel Upregulated	97	1.1	Endochitinase	68.5	731	Oriza sativa X56063
SEQ -ID-NO-28	Peel Upregulated	20	0.7	Beta-1,3-Glucanase	61.9	754	Hordeum vulgare M96939
SEQ -ID-NO-29	Peel Upregulated	33	1.2	Beta-1,3-Glucanase	60.1	697	Barley M91814

Sequence Identity	Group	Clone no.	Size Kb	Gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-30	Peel Upregulated	36	1.2	Beta-1,3-Glucanase	61.4	720	Barley M91814
SEQ -ID-NO-31	Peel Upregulated	53	1.2	Beta-1,3-Glucanase	57.3	592	Nicotiana plumbaginifolia M63634
SEQ -ID-NO-32	Peel Upregulated	58	1.3	Beta-1,3-Glucanase	59.8	716	Hordeum vulgare M96939
SEQ -ID-NO-33	Peel Upregulated	72	0.8	Beta-(1,3;1,4)-D-Glucanase	62.7	585	Barley X52572
SEQ -ID-NO-34	Peel Upregulated	86	1.2	Beta-1,3-Glucanase	58.9	638	Hordeum vulgare M96939
SEQ -ID-NO-35	Peel Upregulated	96	1.1	Beta-1,3-Glucanase	61	703	Hordeum vulgare M96939
SEQ -ID-NO-36	Peel Upregulated	100	1.1	Beta-glucanase	59.5	639	Nicotiana plumbaginifolia M23120
SEQ -ID-NO-37	Peel Upregulated	102	1.1	Beta-1,3-Glucanase	59.8	487	Nicotiana plumbaginifolia X07280
SEQ -ID-NO-38	Peel Upregulated	103	1.1	Beta-1,3-Glucanase	57.8	642	Glicine max A26451
SEQ -ID-NO-39	Peel Upregulated	140	1.1	Endo-1,3-beta-glucanase	59.4	647	Hordeum vulgare M96939
SEQ -ID-NO-40	Peel Upregulated	89	1.3	Beta-glucosidase	62	510	Trifolium repens X56733

Sequence Identity	Group	Clone no.	Size Kb	Gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-41	Peel Upregulated	129	1.3, 0.6	Beta-glucosidase	59.1	643	Trifolium repens X56733
SEQ -ID-NO-42	Peel Upregulated	24	0.6, 0.5	UDP glucose pyrophosphorylase	74.8	785	Solanum tuberosum D00667
SEQ -ID-NO-43	Peel Upregulated	26	0.5	Legumin storage protein	63.2	190	Calocedrus decurrens X95539
SEQ -ID-NO-44	Peel Upregulated	35	0.6, 0.5	Legumin storage protein	63.2	190	Calocedrus decurrens X95540
SEQ -ID-NO-45	Peel Upregulated	63	0.5	Legumin storage protein	51.7	526	Magnolia salicifolia X82465
SEQ -ID-NO-46	Peel Upregulated	29	1	Isoflavonoid Reductase	59.3	735	Arabidopsis thaliana Z49777
SEQ -ID-NO-47	Peel Upregulated	93	1	Isoflavonoid Reductase	63	692	Solanum tuberosum X92075
SEQ -ID-NO-48	Peel Upregulated	39	1.0.8, 0.7, 0.5	Extensin	57.3	288	Chlamidomonas reinhardtii X16619
SEQ -ID-NO-49	Peel Upregulated	41	1.2	Chitinase	57.5	454	Oriza sativa U02286
SEQ -ID-NO-50	Peel Upregulated	57	3	PEP carboxylase	65.5	537	Glicine max D10717
SEQ -ID-NO-51	Peel Upregulated	109	0.9	Beta-1,3-glucanase regulator gene	54.3	175	Nicotiana plumbaginifolia M63634



Sequence Identity	Group	Clone no.	Size Kb	Gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-52	Peel Upregulated	134	2.5, 0.6	High Mobility Group protein	67.3	483	Zea mays X58282
SEQ -ID-NO-53	Peel Upregulated	37	1.1, 0.7	Unknown	-	-	-
SEQ -ID-NO-54	Peel Upregulated	42	2.3	Unknown	-	-	-
SEQ -ID-NO-55	Peel Upregulated	47	1	Unknown	-	-	-
SEQ -ID-NO-56	Peel Upregulated	48	3.7	Unknown	-	-	-
SEQ -ID-NO-57	Peel Upregulated	54	1.3, 0.7	Unknown	-	-	-
SEQ -ID-NO-58	Peel Upregulated	66	0.8, 0.7	Unknown	-	-	-
SEQ -ID-NO-59	Peel Upregulated	84	1.5, 0.6	unknown	-	-	-
SEQ -ID-NO-60	Peel Upregulated	96	1.4	unknown	-	-	-
SEQ -ID-NO-61	Peel Upregulated	97	1.1	unknown	-	-	-
SEQ -ID-NO-62	Peel Upregulated	98	1.8	unknown	-	-	-

Sequence Identity	Group	Clone no.	Size Kb	Gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-63	Peel Upregulated	112	1, 0.6	unknown	-	-	-
SEQ -ID-NO-64	Peel Down regulated	24	3	Elongation factor EF1-alpha	54.1	268	Porphyra purpurea U08841
SEQ -ID-NO-65	Peel Down regulated	28	1.3	Unknown	-	-	-
SEQ -ID-NO-66	Peel Down regulated	86	1.7, 0.5	Elongation Factor 1-alpha	80.6	708	Hordeum vulgare Z23130
SEQ -ID-NO-67	Peel Down regulated	38	2.5	Heat Shock Protein	87.2	218	Oriza sativa X67711
SEQ -ID-NO-68	Peel Down regulated	88	0.9	Histone H1	60.1	619	Zea mays X57077
SEQ -ID-NO-69	Peel Down regulated	141	1.8, 0.8	Wali 7	66.4	432	Triticum aestivum L28008
SEQ -ID-NO-70	Peel Down regulated	60	2.3	Unknown	-	-	-

Sequence Identity	Group	Clone no.	Size Kb	Gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-71	Peel Down regulated	92	3.5	Unknown	-	-	-
SEQ -ID-NO-72	Peel Down regulated	110	0.5	Unknown	-	-	-
SEQ -ID-NO-73	Peel Down regulated	123	0.8	Unknown	-	-	-

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: ZENECA LIMITED  
 (B) STREET: 15 STANHOPE GATE  
 (C) CITY: LONDON  
 (D) STATE: LONDON  
 (E) COUNTRY: UNITED KINGDOM  
 (F) POSTAL CODE (ZIP): W1Y 6LN

(ii) TITLE OF INVENTION: GENTIC CONTROL OF FRUIT RIPENING

(iii) NUMBER OF SEQUENCES: 73

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:  
 APPLICATION NUMBER:

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 809 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-7

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCACGAGCAA TCAGGGAAAG AAAGAGCGTG TCATGGATTC CTTTCCGGTT ATCGACATGG	60
AGAAGCTTTT GGGAAGGGAG AGAGGAGCAG CCATGGAGAT CCTCCGAGAT GCTTGCGAGA	120
AATGGGGCTT CTTTGAGATT TTAAACCATG GCATCTCACA TTACCTCATG GATGAAGTGG	180
AGAAGGTGAA CAAAGAACAG TACAACAAAT GCAGGGAGCA AAAGTTCAAC GAGTTCGCCA	240
ACAAAGCACT GGAAACGCC GACTCAGAAA TCGATCACCT CGACTGGGAA AGCACCTTTT	300
TCCTGCGTCA TCTCCCCGTC TCCAACATTT CTGAGATCCC CGATCTTGAT GACCAGTATA	360
GGAAGGCGAT GAAGGAATTT GCTGCAGCGA TAGAAGAAGC TGGCAGAGCG GCTGCTCGAC	420
TTGCTGGGTG AGAACCTGGA GCTGGAGAAG GGGTACCTGA AGAAAGCCTT CTCTAATGGA	480
TCCAAGGGGC CAACCTTTGG GACCAAGGTC AGCAGCTACC CGCCATGCCC GCGCCCGGAC	540
CTGGTGAAGG GCCTGAGGGC GCACACCCGA CGCCGGGANG CATCATCTTG CTCTTCCANG	600
AAGAACANGT CAGCGGCCTG CAGTTCCTC AAGGACGGCG AATTGGCTGG ACTTNCCCCC	660
CATGCGCCAC GCCATCGTCG TCAACCTCNG CGAACAGCTC CAAGGTANTC CNCAATGGCA	720
AGTTCAAAAC NTTGGTGCCC CGCCTTGGTT GGCTCNAAT GATGGCAACN GGATNTCAAT	780
GNCTCCCTCC TACACCCCGG GAACNANCC	809

## (2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 736 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-13

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGCACGAGGT GCAATCAGGG AAAGAAAGAG CGTGTCATGG ATTCCTTTCC GGTATATCGAC	60
ATGGAGAAGC TTTTGGGAAG GGAGAGAGGA GCAGCCATGG AGATCCTCCG AGATGCTTGC	120
GAGAAATGGG GCTTCTTTGA GATTTTAAAC CATGGCATCT CACATTACCT CATGGATGAA	180
GTGGAGAAGG TGAACAAAGA ACAGTACAAC AAATGCAGGG AGCAAAAGTT CAACGAGTTC	240
GCCAACAAAG CACTGGAAAA CGCCGACTCA GAAATCGATC ACCTCGACTG GGAAAGCACC	300
TTTTTCCTGC GTCATCTCCC CGTCTCCAAC ATTTCTGAGA TCCCGATCT TGATGACCAN	360
TATAGGAAGG CGATGAAGGA ATTTGCTGCA GCGATAGAGA AGCTGGCAGA GCGGCTGCTC	420
GACTTGCTGG GTGAGAACCT GGAGCTGGAG AAGGGGTNCC TGAANAAAGC CTTTCTCTAA	480
TGGATCCAAG GGGCCAACCT TTGGGACCAA GGTCAGCATC TACCCGCCAT GCGCGCGCCC	540
GGACCTGGTG AANGGCCTGA GGGCGCCAC CCGACGCCG ANGCACTNTC TTGCTCTTCC	600
AGGAAGAACA NGTCTCCGGC CTGCNNTTCC TCAAGGACGG CAANTGGCTT GGACTIONCCC	660
CCCATGCGCC NCGCCATCGT CGTTCNACCT TCNGCGAACA NGCTCGANGT TATCCCCAAT	720
TGGCTAGTTC NANAAC	736

## (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 787 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-23

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CACGAGCACA AGTGCAATCA GGGAAAGAAA GAGCGTGTCA TGGATTCTT TCCGGTTATC	60
GACATGGAGA AGCTTTTGGG AAGGGAGAGA GGAGCAGCCA TGGAGATCCT CCGAGATGCT	120
TGCCAGAAAT GGGGCTTCTT TGAGATTTTA AACCATGGCA TCTCACATGA CCTCATGGAT	180
GAAGTGGAGA AGGTGAACAA AGAACAGTAC AACAAATGCA GGGAGCAAAA GTTCAACGAG	240
TTCGCCAACA AAGCACTGGA AAACGCCGAC TCAGAAATCG ACCACCTCGA CTGGGAAAGC	300

ACCTTTTTCC TCGTCATCT CCCCGTCTCC AACATTTCTG AGATCCCCGA TCTTGATGAC 360  
 CAGTATAGGA AGGCGATGAA GGTAATTTGC TGCAGCGATA GAGAAGCTGG CAGAGCGGCT 420  
 GCTCGACTTG CTGGGTGAGA ACCTGGAGCT GGAGAAGGGG TACCTGAAAG AAAGCCTTCT 480  
 CTAATGGATC CAAGGGGCCA ACCTTTGGGA CCAAGGTCAG CAGCTACCCA CCATGCCCCAC 540  
 GCGCGACCT GGTGAAGGGC CTTGAGGGCG CACNCCGACG CCGGAGGCAT CATCTTGCTC 600  
 TTCCAGGACG AACANGTCNG CGGCCTGCAG TCCTCAAGGA CGGCGAATGG CTGGACTNCC 660  
 CCCCCATGCG CCATGCCATC GTCCTCAACC TCGGCGACAG CTCGAAGTAA TCCCCAATGG 720  
 CAATTACAAA ACGTTGGTGC ACCGCNTTGG TGGCCAAACT GATGGCACNG GATGTCAATT 780  
 GCTCCTC 787

## (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 736 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-105

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CACGAGCACA AGTGCAATCA GGGAAAGAAA GAGCGTGTC TGGATTCCTT TCCGGTTATC 60  
 GACATGGAGA AGCTTTTGGG AAGGGAGAGA GGAGCAGCCA TGGAGATCCT CCGAGATGCT 120  
 TGCGAGAAAT GGGGCTTCTT TGACATTTTA AACCATGGCA TCTCACATGA CCTCATGGAT 180  
 GAAGTGGAGA AGGTGAACAA AGAACAGTAC AACAAATGCA GGGAGCAAAA GTTCAACGAG 240  
 TTCGCCAACA AAGCACTGGA AAACGCCGAC TCAGAAATCG ACCACCTCGA CTGGGAAAGC 300  
 ACCTTTTTCC TCGTCATCT CCCCGTCTCC AACATTTCTG AGATCCCCGA TCTTGATGAC 360  
 CAGTATAGGA AGGCGATGAA GGAATTTGC TGCAGCCGAT AGANAAGCTG GCNGAGCGGC 420  
 TGCTCCNACT TGCTGGGTTG AGAACCTGGA GCTGGGAGAA GGGGTNCCTG AAAGAAAGCC 480  
 TTCTCTAATG GGATCCAAGG GGCCAACCTT TTGGGGACCA AGGTCAGCNG CTTACCCAC 540  
 CATGCCCCAC GCGCGACCT GGTGAANGGC CTGAAGGCGC NCTCCGACGC CCGGGANGCA 600  
 TCATCTTGCT CTTCCAAGAA CGAACAGGTC NNCGGGCTGC AGTTCCTCCA GGACGGCGAA 660  
 TGGCTGGACT TNCCTCATG CCGCCATGCC ATCGTCGTNC ACCTCGGGGA ACNGCTCGAN 720  
 GTATCCCCCA TGGCAA 736

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 823 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCGGCAGCAA GCTGGCTGGG GTGTTGGTGG AATTGAGGCA GAAGCCGCAA TGCTTGCCCA	60
GCCGATGAGC ATGGTACTGC CTGGAGTTGT TGGTTTCAAA CTTGGTGGAA AATTGAGGAA	120
TGGTGTGACC GCTACAGACT TGGTCTGAC TGTGACCCAN ATGCTTCGGA AGCATGGAGT	180
CGTTGGGAAG TTTGTTGAGT TTTATGGAGA AGGCATGAGT GAACTTTCTT TAGCAGATCG	240
TGCCACTATT GCAAATATGT CCCCTGAGTA TGGAGCAACT ATGGGTTTCT TCCCAGTTGA	300
CCATGTCACA CTGCAGTATT TGAACTGAC TGGAAGAAGT GATGAGACTG TGGCCATGAT	360
AGAAACATAC TTACGAGCCA ATAAAATGTT TGTTGACTAC AGTCAGCCAC AAAGTGAAAG	420
AGTATACTCA TCTTATTTGG AGTTGAAATC TGGAAGATGT NNAACCATGC ATATCAGGAC	480
CTAAAAGGCC TCATGATCGA NTCCCTTTGA AGGGAATGAA ATCNNATTGG CAGACTTGTT	540
TANACNACAA ANTTGGCTTC AAGGGTTTGG CTGTGCCANA AGAACCAGAG ACAAATTCG	600
AGAATTTTTC TTTCCGTGGT ACACCTGCCC ANATNAANCA TGGTGATGTT GTGATTGGCT	660
GCAATTACCN GTTGACGAA CACATCCAAT CCTAATGTTA TGCCTTGGA CTGCTTTGGT	720
TNCCAAAAAA NGCTNGTTGA ACTGGGTCTT GAAGTGAACC CCTGGATTAA GAATAATCCT	780
NCCCCANGTT CCTGGANTTG TTGACAAATN CCTGGAAAAA AAT	823

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 749 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCAGGANAC AAAAATGGCA GCATTCATGT TCTTCCTCAC CATCGCAGCC TTCACTGCCC	60
CCGTCTACTC TTCTCGTGCA CCCTTAACGT CAGCAGCTGT CCGCGACCCT GAATTAGTAG	120
TACAGGAAGT ACAAAGAAGC TTGAACGTGT CGCGCGGGCG ACTGGGCTAC TTGTCATGCG	180
GCACCGGCAA TCCGATCGAC GACTGCTGGC GGTGCGACCC TGAAGGGCT GACAACCGGC	240
AGCGGCTCGC TGAAGTGGCC ATCGGGTTCG GGAAGAAGCG GATTGGGGG AGGGACGGCG	300
AGATATACNT GGTGACCGAC AGTGCGCAGC ACNACCCCGT CAATCCGAAA ACGGGCACGC	360
TCCGGTACGC CGTCATCCAG GAGGAGCCGC TGTGGATCAT CTTCAAGCGC GACATGGTCA	420
TCCAGCTGAA AGGAGGAAGC TCATCATGAA CTCCACAAG ACCATCGACG GCCGGGGCGC	480
CAGCGTCCAC ATCTCCGGCG GGCCGTGCAT CACCATCCAG TACGTCACCA ACATCNTCAT	540

CCACGGCGTC CACATCCACN ACTGCAAGCA GGGCGGGAAC GCGTTNCGTG CGCGACNCCC	600
CANGGCACTA CNGGTGGCGC ACGGTGTCNG ACGCGACGGG TNTTCCATCT TCNGCGGNA	660
NCCACTTCTT GGGTCCAACA ACTGCCNCNC TGTCCAATG CCACCAATGG CCTCATCNAC	720
CCCATTCCNT NGGATNCCCC NCCAATTAC	749

## (2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 704 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: U-12

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGAGCTTCGA TCACATCTTT TTGCTCTGGG AAACGTGAGA GGTGAGACGA GGGCGGCAAT	60
GACGGCGGGT TTAANATGGA TTCCTCCTCT GCTTCTTCTT CTTATGGGCT TCCTGCTGGT	120
TTTGAACGGA GGTCTGGGGT GGATTGGAAG CGAGAGGTCC TCTGGCTCGA GGAATGGCGG	180
AGCATCNCGG AGGAGCTTGA GAGAGGCCTC CGCGAACGCG ACCAGCGCCG ATGCTTCCTT	240
GGAAGACAGG GCTGTNACCA GGGCAGCAGA AGCCGAGTC NATGACCCG AGGAGGTTGC	300
TTCNACGGTC CTGACGACCA TAATCAACAG CACGGCTCGA AAATCTCTTG GTTATCTGTC	360
GTGCGGTCA GGCAACCCGA TCGACNACTG CTGGCGGTGC GACCCCGATT GGCATGTCAA	420
CAGAAAAAAA GCTCNCTGAC TGTGGCATTG GCTTTGGCCG CAACGCCATA NGTGGCCGCG	480
ACGGGGANTT GTACNTTGTG ACAGACTCCG GGGACGATGA TCCCGTGAAT CCTCNCCTCG	540
GAACACTTAN ATACNCCCGT CANCCANGA AGTGCCCTC TGGGATCNCC TTAAACCCC	600
ACNTNGANAT CTCCGCTCNA NGGANGAACT CATTTATGAA CNTCTTTTAA NAACAATCCA	660
ATGGACNCCN GTGTCCACCT CCACNTTGC CANTGGCGCC TCCC	704

## (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 793 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: U-22

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CACGAGCTGT TCTCTCCTTC GATCACATCT TTTTGCTCTG GGAAACGTGA GAGGTGAGAC	60
GAGGGCGGCA ATGACGGCGG GTTAAAGATG GATTCTCCT CTGCTTCTTC TTCTTATGGG	120



CTTCCTGCTG GTTTTGAACG GAGGTCGGGG GTGGATTGGA AGCGAGAGGT CCTCTGGCTC	180
GAGGAATGGC GGAGCATCGC GGAGGAGCTT GAGAGAGGCC TCCGCGAACG CGACCAGCGC	240
CGATGCTTCC TTGGAAGACA GGGCTGTAAC CAGGGCAGCA GAAGCCGCAG TCGATGACCC	300
CGAGGAGGTT GCTTCGACGG TCCTGACGAC CATAATCAAC AGCACGGCTC GAANATCTCT	360
TGGTTATCTG TCGTGC GGTT CAGGCAACCC GATCGACGAC TGCTGGCGGT GCGACCCCGA	420
TTGGCATGTC AACAGAAAAA AAGCTCGCTG ACTGTGGCAT TGGCTTTGGC CGCAACGCGA	480
TAGGTGGCCG CGACGGGGAN TTGTNCGTTG TGACAGACTC CGGGGACGAT GATCCCGTGA	540
ATCCTCGCCC GGGGAACACT TANATACGCC GTCNTCCANG ACGTGCCCTT CTGGATCACC	600
TTTAAACACG ACATGGAAAT CACCTCCAGG AAGAACTCNT TATGAACNGC TTTAANACAA	660
TCGATGGACC CGTGTACGT CCACATTGCC AATGGCGCCT GCTTCACCAT CCAATTAATC	720
ACCAACNTCA TCNTCCATGG CCTCCACNTC CACAAATGCN ACCCACCNGG AATNCCTTGG	780
TCCCACTCTC TTC	793

## (2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 708 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-31

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ACGAGGGAGA ACAAAAATGG CAGCATTCCT GTTCTTCCTC ACCATCGCAG CCTTCACTGC	60
CCCCATCTAC TCTTCTCGTG CACCCTTAAC GTCGGCAGCT GTCCGCGACC CTGAATTAGT	120
AGTACAGGAA GTACAAAGAA GCTTGAACGT GTCGCGGCGG CGACTGGGCT ACTTGTCATG	180
CGGCACCGGC AATCCGATCG ACGACTGCTG GCGGTGCGAC CCTGACTGGG CTGACAACCG	240
GCAGCGGCTC GCGGACTGCG CCATCGGGTT CGGGAAGAAC GCGATTGGGG GCANGGACGG	300
CGANATATAC GTGGTGACCG ACAGTGGCGA CNACNACCCC GTCAATCCGA AGCCGGGCAC	360
GCTCCGGTAC GCCGTCATCC ANGAGGAGCC GCTGTGGATC ATCTTCAAGC GCGACATGGT	420
CATCCANCTG AAGGAGGAGC TCATCCNTGA ACTCCACAA GACCNTCNAC GGCCGGGGCG	480
CCAGCGTCCA CATCTCCGGC GGGCCGTGCA TCACCATCCA GTTACTTTCTN CCAACATCAT	540
CNTCCACGGC GTCCACATCC ACGACTGCAA TCCANGGCGG GGAACCTCTN CGTTCGCCAC	600
TCCCCCATNG GCACTNCGGG TGGCGCACGG TGTCTGAAGG CGACGGGGTN TTCTTCTTTC	660
CGCGGCAGCC AATTTTTGGG TTCAACTACT GCNCCGCTGT TTCAACTG	708

## (2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 823 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: U-51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ACGAGCGGAG AACAAAAATG GCAGCATTCT TGTTCTTCCT CACCATCGCA GCCTTCACTG	60
CCCCCGTCTA CTCTTCTCGT GCACCCTTAA CGTCAGCAGC TGTCCGCGAC CCTGAATTAG	120
TAGTACAGGA AGTACAAAGC TTGAACGTGT CGCGGCGGCG ACTGGGCTAC TTGTCATGCG	180
GCACCGGCAA TCCGATCGAC GACTGCTGGC GGTGCGATCC TGACTGGGCC GACAACCGGC	240
AGCGGCTCGC GGAATGCGCC ATCGGGTTCG GGAAGAACGC GATTGGGGGG AGGGACGGCG	300
AGATATACGT GGTGACCGAC AGTGGCGACG ACGACCCCGT CAATCCGAAG CCGGGCACGC	360
TCCGGTACGC CGTCATCCAG GAGGGAGCCG CTGTGGATCA TCTTCAAGCG CGACATGGTC	420
ATCCAGTTGA AGGAGGAGCT CATCATGAAC TCCCACAAGA CCATCGACGG CCGGGGCGCC	480
AGCGTCCACA TCTCCGGCGG GCCGTGCATC ACCATCCCAG TACGTCACCA ACATCATCAT	540
CCACGGCGTC CACATCCACG ACTGCAAGCA GGGCGGGAAC GCNTACGTTG CGCGACTCCC	600
CAGGGCACTA CGGGTTGGCG CNCGGTGTGN GACGGCGACG GGGTTTCCAT CTTCGGCGGG	660
AGCCACTTCT GGGTCNACCA CTGCCCTGTC CAACTGCCAC AACGGCCTCN TCNACNCCNT	720
TCTTGGATTG NCCGCNATCC CCATTTTCCA ACAACTACTT GANCCNCCNT GACAAGGTCT	780
TGCNGCTNGG TCCCANCAAT AATTGACTTC CNACAAAAC TGC	823

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 745 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: U-52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ACGAGCTGTT CTCTCCTTCG ATCACATCTT TTTGCTCTGG GAAACGTGAG AGGTGAGACG	60
AGGGCGGCAA TGACGGCGGG TTTAAGATGG ATTCTCTCTC TGCTTCTTCT TCTTCTGGGC	120
TTCTCTGCTGG TTTTGAACGG AGGTCGGGGG TGGATTGGAA GCGAGAGGTC CTCTGGCTCG	180
AGGAATGGCG GAGCATCGCG GAGGAGCTTG AGAGAGGCCT CCGCGAACGC GACCAGCGCC	240
GATGCTTCCT TGGAAGANAG GGCTGTAACC CGGGCAGCAG AAGCCGCAGT CGACGACCCC	300
GAGGAGGTTG CTTGACGGT CCTGATGACC ATAATCAACA GCACGGCTCG CANATCTCTT	360
GGTTATCTGT CGTGCGGTTC AGGCAACCCG ATCGACNACT GCTGGCGGTG CGACCCGTAT	420

TGGCNTGTCA ACAGAAAAA AGCTCGCTGA CTGCGGCATT GGCTTTGGAC GCAACGCNAT	480
NGGTGGCCGC NACGGGGANT TGTACGTTGT GACAGACTCC GGGGACNATG ATCCCGTGAA	540
TCCTCNCCCG GGAACNCTTA NATACGCCGT CATCCANGAC GTGCCCCTCT GGATCACCTT	600
TAAACACNAC ATGGANATCA CCCTCNAGGN AGGAACTCCT TTATGAAACN GCTTTTNACA	660
ACATCGATGG ACCCGTGTTT CNCNTCCACA TTGCCAATGG CGCCTGCTTC ACCATCCNAT	720
TACATCACCA ACGTCATCCT CCATG	745

## (2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 758 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: U-57

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ACGAAGGAAG AACAAANATG GCAGCATTCT TGTTCTTCCT CACCATCGCA GCCTTCACTG	60
CCCCCATCTA CTCTTCTCGT GCACCCCTTAA CGTCGGCAGC TGTCCGCGAC CCTGAATTAN	120
TAGTACAGGA AGTACAAAGA AGCTTGAACG TGTCGCGGCG GCGACTGGGC TACTTGTCAT	180
GCGGCACCGG CAATCCGATC GACGACTGCT GCGGGTGCGA CCCTGACTGG GCTGACAACC	240
GGCAGCGGCT CGCGGACTGC GCCATCGGGT TCGGGAAGAA CGCGATTGGG GGCAGGGACG	300
GNGANATATA CGTGGTGACC GACAGTGGCN ACGACGACCC CGTCNATCCG AANCCGGGCN	360
CGCTCCGGTA CGCCGTCATC CAGGAGGAAG CCGCTGTGGG ATCATCTCCA AGCGCGACAT	420
GGTCATCCAT CTNAAGGAGG AANCTCATCA TGAAACTCCC ACAANACCCA TCTACGGGNC	480
GGGGCGCCAG CNTCCATATC TCCNGCGGGC CGTGCATCAC CATCCTGTAC TTCACCAACA	540
TCATCATCCA CGGCGTCCAC TTCCACNACT GCTTNCCAGG GCGGGAACNC TTNCTTNCGC	600
GACTCCCCC NGTGGCACTA CNGGNTGGNC GCTCNGTGT CTGAACGGCN ACGGGGGTGT	660
TCCTTCTTCT GCCGGGCATC CCCCCTCCTG GGTCCNNCNC TTGCCNCCTC TTTTCCTTAC	720
TNCCTNTCAC GGGCNTCCTC CAACCCNTTC CTNNNTT	758

## (2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 794 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: U-59

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CACGAGCGGA GAACAAAAAT GGCAGCATTC TTGTTCTTCC TCACCATCGC AGCCTTCACT	60
GCCCCCGTCT ACTCTTCTCG TGCACCCTTA ACGTCAGCAG CTGTCCGCGA CCCTGAATTA	120
GTAGTACAGG AAGTACAAAG AAGCTTGAAC GTGTCGCGGC GCGGACTGGG CTACTTGTC	180
TGCGGCACCG GCAATCCGAT CGACGACTGC TGGCGGTGCG ATCCTGACTG GGCCGACAAC	240
CGGCAGCGGC TCGCGGACTG CGCCATCGGG TTCGGGAAGA ACGCGATTGG GGGGAGGGAC	300
GGCGAGATAT ACGTGGTGAC CGACAGTGGC GACGACGACC CCGTCAATCC GAAGCCGGGC	360
ACGCTCCGGT ACGCCGTCAT CCAGGAGGAA GCCGCTGTGG ATCATCTTCA AGCGCCGACA	420
TGGTCATCCA GTTGAAGGAG GAGCTCATCA TGAAGTCCCA CAAAGACCAT CGACGGGCGG	480
GGCGCCAGCG TCCACATCTC CGGCGGGCCG TGCATACCA TCCAGTACGT CACCAACNTC	540
ATCATCCACG GGGTCCACAT CCACNANTGC AANCAGGGCG GGAACGCGTA CTNCGCCNAC	600
TCCCANGGCA CTNCGGGTTG CGCACGGTGT CGGAACGGCN AAGGGGTNTT CCATCTTCCC	660
GGGGGNAGCC CCNTTCTGGG TCAACACTTG CNCCCTTTCC AACTGGCCCC AAACGGCCTN	720
CTCCAACCCC TTTCTGGAT TCCCCCCGA NTCCCNNTT TCCACNNNTT CNTTGAACCC	780
CCCNTGAANA NGGT	794

## (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 710 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-68

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CAGCATTCAT GTTCTTCCTC ACCATCGCAG CCTTCACTGC CCCCCTCTAC TCTTCTCGTG	60
CACCCTTAAC GTCAGCAGCT GTCCGCGACC CTGAATTAGT AGTACAGGAA GTACAAAGAA	120
GCTTGAACGT GTCGCGGCGG CGACTGGGCT ACTTGTCATG CGGCACCGGC AATCCGATCG	180
ACGACTGCTG GCGGTGCGAC CCTGACTGGG CTGACAACCG GCAGCGGCTC GCTGACTGCG	240
CCATCGGGTT CGGGAAGAAC GCGATTGGGG GCAGGGACGG CGAGATATAC GTGGTGACCG	300
ACAGTGGCGA CGACGACCCC GTCAATCCGA AAACGGGCAC GCTCCGGTAC GCCGTCATCC	360
AGGAGGAGCC GCTGTGGATC ATCTTCAAGC GCCGACATGG TCATCCAGCT TGAAGGAGGA	420
GCTCATCATG AACTCCACA AGACCATCCN ACNCCGGGG CGCCAGCGTC CNCNTCTCCG	480
GGGGGCCGTG GCATCACCAT CCATTACGT TCTCCAACAT TCNTCATCCN CNGGNGTTCC	540
AACATCCACN AACTGCNANC TNGGCGGGGA AANNNTTTCG TTNCCGCNAC TCCCCAAGGG	600
CNCTAACGGG TTGGCNCACG GTGTCNGAAC GGCAACGGGG TTTTCCTTCT TCGGCGGGCA	660
NTNCNCCTTC TNGGGTCNAA CTTCTGCCCC CCGTTCCAA CTNGCCNCAA	710

## (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 745 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-69

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CACNAGGCCC CCGTCTACTC TTCTCGTGCA CCCTTAACGT CAGCAGCTGT CCGCGACCCT	60
GAATTAGTAG TACAGGAAGT ACAAAGAAGC TTGAACGTGT CGCGGCGGCG ACTGGGCTAC	120
TTGTCATGCG GCACCGGCAA TCCGATCGAC GACTGCTGGC GGTGCGATCC TGACTGGGCC	180
GACAACCGGC AGCGGCTCGC GGACTGCGCC ATCGGGTTCG GGAAGAACGC GATTGGGGGG	240
AGGGACGGCG AGATATACGT GGTGACCGAC AGTGGCGACG ACGACCCCGT CAATCCGAAG	300
CCGGGCACGC TCCGGTACGC CGTCATCCAG GAGGAAGCCG CTGTGGATCA TCTTCAAGCG	360
CGACATGGTC ATCCAGTTGA AGGAGGAGCT CATCATGAAC TCCCACAAGA CCATCCGACG	420
GCCGGGGCGC CAGCGTCCAC ATCTCCGGCG GGCCGTGCAT CACCATCCAG TACGTCACCA	480
ACATCATCAT CCACGGCGTC CACATCCACG ACTGCAANCA GGGCGGGAAC GCGTACGTGC	540
GCGACTCCCC AAGGCACTNC GGGTTGGCNC ACGGTGTCCG ACGGCNACGG GGTGTCCATC	600
TTCCGCNGCA NCCACNTCTG GGTCAACACT GCNCGCTGTC CACTGCCACA ACGGCTCTTC	660
GACCCNTTC CTGGATTCCC CGCGATTCCC CATTTCCAC AACTACTTNA ACCCCNTGA	720
ANAGGTCCTG CTNCTGGGTC CAACC	745

## (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 731 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-85

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CACGAGGGAG AACAAAAATG GCAGCATTCT TGTCTTCCT CACCATCGCA GCCTTCACTG	60
CCCCCATCTA CTCTTCTCGT GCACCCTTAA CGTCGGCAGC TGTCCGCGAC CCTGAATTAG	120
TAGTACAGGA AGTACAAAGA AGCTTGAACG TGTGCGGGCG GCGACTGGGC TACTTGTCAT	180
GCGGCACCGG CAATCCGATC GACGACTGCT GGCGGTGCGA CCCTGACTGG GCTGACAACC	240
GGCAGCGGCT CGCGGACTGC GCCATCGGGT TCGGGAAGAA CGCGATTGGG GGCAGGGACG	300

GCGAGATATA CGTGGTGACC GACAGTGGCG ACGACGACCC CGTCAATCCG AAGCCGGGCA	360
CGCTCCGGTA CGCCGTCATC CAGGAGGAGC CGCTGTGGAT CATCTTCAAG CGCCGACATG	420
GTCATCCAGC TGAAGGAAGG AGCTCATCCN TGAACTCCCA CAAAGACCAT CGACGGGCGG	480
GGCGCCAGCG TCCACATCTC CGGCGGGGCC GTGCATCACC ATCCANTACG TCACCAACAT	540
CATCATCCAC GGGGTCCACA TCCACNACTG CAACNNGGCG GGAACCCTTA CTTGCGCCAA	600
TCCCCAGGG CNCTNACGGG TTGGCCACGG TGTTCCGACG GCAACGGGGT NTTTCATCTTC	660
CGGCGGGGANC CNCNTCTNGG GTCAACACTT CACNCTTTCC AACTTGCCNC NANNGGCTCN	720
TCCAACCCCN T	731

## (2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 772 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-101

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CACNAGCAAA AATGGCAGCA TTCATGTTCT TCCTCACCAT CGCAGCCTTC ACTGCCCCCG	60
TCTACTCTTC TCGTGCACCC TTAACGTCAG CAGCTGTCCG CGACCCTGAA TTAGTAGTAC	120
AGGAAGTACA AAGAAGCTTG AACGTGTCGC GGC GGCGACT GGGCTACTTG TCATGCGGCA	180
CCGGCAATCC GATCGACGAC TGCTGGCGGT GCGACCCTGA CTGGGCTGAC AACC GGCGAGC	240
GGCTCGCTGA CTGCGCCATC GGGTTCGGGA AGAACGCGAT TGGGGGCAGG GACNGNTATA	300
TNTACGTGGT GACCGACAGT GCGGACGACG ACCCGCTCAA TCCGAAAACG GGCACGCTCC	360
GGTACGCCGT CATCCAGGAG GAGCCGCTGT GGATCATCTT CAAGCGCGAC ATGGTCATCC	420
AGCTGAAAGG AAGGAGCTCA TCATGAACTC CCACAAAGAC CATCGACGGG CGGGGCGCCA	480
GCGTCCACAT CTCCGGCGGG CCGTGATCA CCATCCANTA CGTCACCAAC ATCATCATCC	540
CACGGGGTCC ACATCCACGA ATGCNANCAN GGGNNGGAAC GCGTNCGTGC GCGACTCCCC	600
CAGGGCACTA CGGGTTGGCG CACGGTGTG GACGGCNAAN GGGTTTCCAT CTTTCNGCNG	660
GAGCCACTTC TGGGGTCGAA CAANTGCNCG CCTGTCCAAC TGGCCACCAA TGGGCNTCCT	720
NCAACCCCTT TCNTNGGATT CCACGCGAT CNCCATTTC CAACAACCTTA CT	772

## (2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 748 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:

(B) CLONE: U-113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CACGAGCAGC TTTTCTGTTC TCTCCTTCGA TCACATCTTT TTGCTCTGGG AAACGTGAGA	60
GGTGAGAAGA GGGCGGCAAT GACGGCGGGT TTAAGATGGA TTCCTCCTCT GCTTCTTCTT	120
CTTCTGGGCT TCCTGCTGGT TTTGAACGGA AGTCGGGGGT GGATTGGAAG CGAGCGGTCC	180
TCTGGCTCGA GGAATGGCGG AGCATCGCGG AGGAGCTTGA GAGAGGCCTC CGCGAACGCG	240
ACCAGCGCCG ATGCTTCCTT GGAAGAGAGG GCTGTAACCA GGGCAGCAGA AGCCGCAGTC	300
GACGACCCCG AGGAGGTTGC TTCGACGGTC CTGACGACCA TAATCAACAG CACGGCTCGC	360
AGATCTCTTG GTTATCTGTC GTGCGGTTCA GGCAACCCGA TCGACGACTG CTGGCGGTGC	420
GACCCCGATT GGCATGTCAA CAGAAAAAAG CTCGCTGACT GCGGCATTGG CTTTGGCCGC	480
AACGCGATAG GTGGCCGCGA CGGGGANTTG TACGTTGTTG ACAGACTCCG GGGACNATGA	540
TCCCCGTGAA TCCTCCCCCG GGAACACTTA NATACGCCGT CATCCANGAC TGCCCCCTCTG	600
GATCNCCTTT AAACACCACN TGGANATCAC CCTCCAGGAA GAACTCNTTA TGAACAGCTT	660
TAAACAATC GATGGACCCG TGTTACGTC CACTTTGCCA ATGGCCCTGC NTCACCATCC	720
ANTNCNTCAC CACNTCTTCN TCCACGGC	748

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 706 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CACNAGGTTC TCTCCTTCGA TCACATCTTT TTGCTCTGGG AAACGTGAGA GGTGAGAAGA	60
GGGCGGCAAT GACGGCGGGT TTAAGATGGA TTCCTCCTCT GCTTCTTCTT CTTCTGGGCT	120
TCCTGCTGGT TTTGAACGGA AGTCGGGGGT GGATTGGAAG CGAGCGGTCC TCTGGCTCGA	180
GGAATGGCGG AGCATCGCGG AGGAGCTTGA GAGAGGCCTC CGCGAACGCG ACCAGCGCCG	240
ATGCTTCCTT GGAAGAGAGG GCTGTAACCA GGGCAGCAGA AGCCGCNNTC NACTACCCCG	300
AGGAGGTTGC TTCGACGGTC CTGACGACCA TAATCAACAG CACGGCTCGC AGATCTCTTG	360
GTTATCTGTC GTGCGGTTCA GGCAACCCCG ATCGACGACT GCTGGCGGTG CCGACCCCGA	420
TTGGCATGTC AACAGAAAAA AGCTCGCTGA CTGCGGCATT GGCTTTTGGC CGCANCGCNA	480
TATGTGGCCG CCGACCGGGG ANATTGTTTCG TTGTTGACAN ACTCCGGGGG ACGATGATCC	540
CGTGAAATCC TCCCCCGGG GAACACTTAN ATNCNCCGTC ATCCAANGAC GTTGCCCTCT	600
GGATCNCCTT TAAACACNAC NTGAAATCA CCCTCCNNGA AGAACTCCTT ATGAACACTT	660

TAANACATCC AATGGNCNCN GTGTCACGTC CACATTTGCC NATGGC

706

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 728 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CACGAGAAAA TGGCAGCATT CTTGTTCTTC CTCACCATCG CAGCCTTCAC TGCCCCCGTC	60
TACTCTTCTC GTGCACCCTT AACGTCAGCA GCTGTCCGCG ACCCTGAATT AGTAGTACAG	120
GAAGTACAAA GAAGCTTGAA CGTGTGCGCG CGGCGACTGG GCTACTTGTC ATGCGGCACC	180
GGCAATCCGA TCGACGACTG CTGGCGGTGC GATCCTGACT GGGCCGACAA CCGGCAGCGG	240
CTCGCGGACT GCGCCATCGG GTTCGGGAAG AACGCGATTG GGGGGAGGGA CGGCGAGATA	300
TACGTGGTGA CCGACAGTGG CGACGACGAC CCCGTCAATC CGAAGCCGGG CACGCTCCGG	360
TACGCCGTCA TCCAGGAGGG AGCCGCTGTG GATCATCTTC AAGCGCGACA TGGTCATCCA	420
GTTTGAAGGA GGAGCTCATC ATGAACTCC CACAAAGACC ATCCGACGGG CGGGGCGCCA	480
GCGTCCACAT CTCGGCGGG CCGTGCATCA CCATCCAGTA CGTCACCAAC ATCATCATCC	540
ACGGGGTCCA CATCCACGAA TGCAANCAGG GCGGGAACGC GTNCGTTGCG CCACTCCCCA	600
AGGCACTACN GGTGGCGCAC GGTGTGCGAC NGCGACGGGT GTCCATCTTT CCGCGGCAGC	660
CACGTTCTGG GTCGAACAAC TGCNCGCTGT CCAACTTGCC ACAACGGCTC NTCCAACCCA	720
TTCCTGGA	728

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 727 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CACGAGCAGC TTTTCTGTTC TCTCCTTCGA TCACATCTTT TTGCTCTGGG AAACGTGAGA	60
GGTGAGAAGA GGGCGGCAAT GACGGCGGGT TTAAGATGGA TTCCTCCTCT GCTTCTTCTT	120
CTTCTGGGCT TCCTGCTGGT TTTGAACGGA AGTCGGGGGT GGATTGGAAG CGAGCGGTCC	180
TCTGGCTCGA GGAATGGCGG AGCATCGCGG AGGAGCTTGA GAGAGGCCTC CGCGAACGCG	240



ACCAGCGCCG ATGCTTCCTT GGAAGAGAGG GCTGTAACCA GGGCAGCAGA ANCCGCNNTC	300
GACGACCCCG AGGAGGTTGC TTCGACGGTC CTGACGACCA TAATCNACAG CACGGCTCGC	360
AGATCTCTTG GTTATCTGTC GTGCGGTTCA GGCNACCCGA TCGACGACTG CTGGCGGTGC	420
GACCCCGGAT TGGCATGTCA ACAGAAAAA GCTCGCTGAC TGCGGCATTG GCTTTGGCCG	480
CAACGCGATA NGTGGCCGCG ACGGGGAATT GTNCNTTGTG ACAGACTCCG GGGACNATGA	540
TCCCGTGAAT CCCTCNCCCG GGAACNCTTA NATACGCCGT CATCCANGAC TNCCCCTCTG	600
GNTCACCTTT TAAACNCCAC ATGGANATCC CGCCCCAGGA AGAACTCATT ATGAACAGCT	660
TTAANACAAT CGATGGACCC GTGTCAACGT TCNCNTTGCC AATGGGGCCT GCNTCNCCNT	720
CCNNTTA	727

## (2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 721 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CACGANCTGG TGCGGTAACA CGGATCCATA CTGCGACAAA GATTGCCAGA GCCAATGCGG	60
CGGTAGCGGC GGTGGCAGCG TGGCCTCGAT CATCAGCTCC TCCCTCTTCG AGCAGATGCT	120
GAAGCATCGC AACGACGCAG CCTGCCCCCG CAAGGGCTTC TACACGTACA CCGCCTTCAT	180
CGCCGCCGCC AACTACTTCA GCGGGTTCGG GACGACCGGC GACGACACCG CGAGGAAGAG	240
GGAGATCGCG GCTTTCTTGG CGCAGACGTC TCACGANACG ACAGGTGGGT GGGCGACGGC	300
TCCCGATGGT CCGTACGCGT GGGGTTACTG CTTCGTCCAG GAACAGAACC CCTCATCGGA	360
CTACTGCGTC GCCAGCTCGC AGTGGCCGTG CGCTGCANGC AATAAATTAC TACGGCCGAG	420
GCCCCATCCA AATCTCATTC AACTACAACCT ACGGGGCCCG CCGGGAANAG CCATCGGCTC	480
CGACCTGCTC AACNACCCAN ACCTGGTGGC CACTGACGCG ACCATCTCCT TCAAGANGGC	540
TCTGTGGTTC TGGATGACTC CTCANTCGCC CAAGCCGTCG TGCCACGACT GATAACCGGG	600
AAGTGGACGC CATCCGACGC CCCAACGGGC GGCCNGAAAG NTTCCGGGC TACNGTNTCC	660
CACCAACATC ATCATTGGAA GGTGGATTT CNGGAAAAGG GTACTATCCA NGGTTGGCCG	720
A	721

## (2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 802 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CACGAATTGT TGTGGTCAT CTTTACCCTG GCCTCGTCCC TCGGCGCCTT CGCCGAGCAA	60
TGCGGAAGGC AAGCCGGGGG GGCTCTCTGC CCCGGCGGGC TGTGCTGTAN CCAGTTCGGC	120
TGGTGCGGTA ACACGGATCC ATACTGCGGC AAANATTGCC ANAGCCAATG CGGCGGTAGC	180
GGCGGTAGCG GCGGTGGCAG CGGTGGCAGC GTTGGCTCGA TCATCAGCTC CTCCCTCTTC	240
GAGCAGATGC TGAAGCATCG CAACGACGCA GCCTGCCCCG GCAAGGGCTT CTACACGTAC	300
AACGCCTTCA TCGCCGCCGC CAACTCCTTC AGCGGGTTCG GGACGACCGG CGACGACNCC	360
ACGAAGAAGA GGGAGATCGC GGCTTTCTTG GCGCANACGT CTCACNAANA CNACAGGTGG	420
GTGGGCGACG GCGCCCGATG GTCCGTACGC GTGGGGTTAC TGCTTCGTCC ANAAAACAGA	480
ACCCCCATC GGACTACTGC GTCNCCAGCT CGCANTGGCC GTGCGCTGCA GGCAANAAGT	540
ACTACGGCCG AAGCCCCATC CAAATCTCAT TCAACTACAA CTACNGGGCC GGCCGGGAAA	600
CCATCGGCTC CGACTGCTCA ACAACCCCAA ACCTGGTGGC CACCGACGCC AACATCTCNT	660
TCAAAANGGC TCTGTGGTTC TGGATAATCT CANTCCCCCA ACCGTCCTNC CACAACTTNA	720
TAACCGGGAA GTGGACCCAT NCCACNCCAA CGGGCNGCCG GAAGGTTCCG GGCTACGGTT	780
TCCCACCAAC ATCNTCATTG GA	802

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 755 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ACGAGCTGGT GCGGTAACAC GGATCCATAC TGCGGCCAAG GATGCCAGAG CCAATGCACA	60
GGCTCCACGC CCTCCCCTTC CACTCCGAGC GGCGGTGGCA GCGTTGGCTC GATCATCAGC	120
TCCTCCCTCT TCGAGCAGAT GCTGAAGCAT CGTAACGACG CAGCCTGCCC CGGCAAGGGC	180
TTCTACACGT ACAACGCCTT CATCGCCGCC GCCAACTCCT TCAGCGGGTT CGGGACTACG	240
GGCGACGACG CCACGAAGAA GAGGGAGATC GCGGCTTTCT TGGCGCAGAC GTCTCAGAN	300
ACGACAGGTG GGTGGTCGAC GGC GCCCGAT GGCCCGTACG CGTGGGGTTA CTGCTTCGTC	360
CAGNAACAGA ACCCTCATC GGACTACTGC GTCNCCAGCT CGCAGTGGCC GTGCGCTGCA	420
GGCAANAATT ACTACGGCCG AGGCCCCATC CAAATCTCAT TCAACTACAA CTACGGGCCG	480
GCCGGGAANA NCCATCGGCT CCGACCTGCT CAACAACCCA NACCTGGTGG CCACCCGACC	540

CNACCATCTC CTTCAANACG GCTCTGTGGT TCTGGGATGA CTCCTCANTC CCCCAGCCG 600  
 TCNTTGCCAC GACGTNATAA CCGGGANCTG GACCCATCCA ACNCCCAACC GGGCNGCCGG 660  
 AAAGGTTTCC NGGTACGGT GTCCCNCCA AATCNTCAAT GGAAGGTTTG GAATTTTCNGG 720  
 AAAGGTCCAA NCCNNGGTGG CNGATANGAT CGGCT 755

## (2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 769 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-54

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACGAAGTCAT CTTTACCCTG GCCTCGTCCC TCGGCGCCTT CGCCGAGCAA TGCGGAAGGC 60  
 AAGCCGGGGG GCTCTCTGCC CCGGCGGGCT GTGCTGTANC CAGTTCGGCT GGTGCGGTAA 120  
 CACGGATCCA TACTGCGGCA AANATTGCCA NAGCCAATGC GCGGTAGCG GCGGTAGCGG 180  
 CGGTGGCAGC GGTGGCAGCG TTGGCTCGAT CATCANCTCC TCCCTCTTCG AGCAGATGCT 240  
 GAAGCATCGC AACGACGCAN CCTGCCCGG CAAGGGCTTC TACACGTACA ACGCCTTCAT 300  
 CGCCGCCGCC AACTCCTTCA GCGGGTTCGG GACGACCGGC GACNACNCCA CCAANAAAAG 360  
 GGAGATCGCG GCTTTCTTGG CGCANACNTC TCACGAAACN ACANGTGGGT GGGCGACNGC 420  
 GCCCGATGGT CCGTACGCGT GGGGTACTG CTTCGTCCAG NAACATAACC CCCCATCGGA 480  
 CTACTGCGTC NCCAGCTCGC ANTGGCCGTG CCCTGCACGC ANTAATTACT TNCGGCCGAA 540  
 GCCCCATCCA AATCTCATTC AACTACAAC ACNGGCCCGG CCGGGAAC CAATCGGCTC 600  
 CGACCTTGCT CCAACAACCC ANACNTGGTG GGCCACCGAC GCGACCATCT CNTTTCAAAA 660  
 ACGGCTCTGT TTGTTCTGGG ATGAANCCTC ANTTCCCCA ANCCTTCTTG CCACNAACTT 720  
 TNATNAACCN GGGANGTGA CGCCATCCCA ACTCCTAAC NGNGCTGGC 769

## (2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 730 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-91

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CACNAGGTTG CTGGTCATTT TTACCCTGGC CTCGTCGCTC GCGCCTTCG CCGAGCAATG 60

CGGAAGGCAA GCCGGGGGGG CTCTCTGCCC CGGCGGGCTG TGCTGTANCC AGTACGGCTG	120
GTGCGGTAAC ACGGATCCAT ACTGCGGCCA AGGATGCCAN AGCCAATGCA CAGGCTCCAC	180
GCCCTCCCCT TCCACTCCGA NCGGCGGTGG CAGCGTTGGC TCGATCATCA GCTCCTCCCT	240
CTTCGAGCAG ATGCTGAAGC ATCGAACGA CGCAGCCTGC CCCGGCAAGG GCTTCTACNC	300
TTNCACCGCC TTCATCGCCG CCGCCAATC CTTAGCGGG TTCGGGACGA CCGGCGACNA	360
CGCCNCCAAN AAGATGGAGA TCGCGGCTTT CTTGGCGCAN ACGTCTCAG AANACNACAG	420
GTGGGTGGTC NACNGCGCCC CGATGGCCCC GTNCGCNTGG GGTACTGCT TCNTCCANGA	480
AACAGAACCC CTCATCGGAC TAACTGCGTC NCCAGCTCCC CANTGNGCCG TGCNCTGCAN	540
GCCANAAATA CTACGGCCGA ANGCCCCATC CNAATCTCCA TTCAACTACA CTACNGGCCG	600
GNCGGGGANA ACCATTNCGC TCCNAACCTG TTCAACAACC CAAAACTGG TTGCCACCG	660
AACCCGANCC ATTCTTCCTT TCAAAAACGG CTCTTTTGGT TCCGGNATAA ATNCTCCAT	720
NNTCCAAACC	730

## (2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 768 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-97

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CACAAGGTTG CTGGTCATTT TTACCCTGGC CTCGTCGCTC GCGCCTTCG CCGAGCAATG	60
CGGAAGGCAA GCCGGGGGGG CTCTCTGCCC CGGCGGGCTG TGCTGTAGCC AGTACGGCTG	120
GTGCGGTAAC ACGGATCCAT ACTGCGGCCA AGGATGCCAG AGCCAATGCA CAGGCTCCAC	180
GCCCTCCCCT TCCACTCCGA GCGGCGGTGG CAGCGTTGGC TCGATCATCA GCTCCTCCCT	240
CTTCGAGCAG ATGCTGAAGC ATCGTAACGA CGCAGCCTGC CCCGGCAAGG GCTTCTACNC	300
NTACAACGCC TTCATCGCCG CCGCCAATC CTTAGCGGG TTCGGGACTA CGGGCGACGA	360
CNCCACGAAN AAAAGGGAGA TCGCGGCTTT CTTGGCGCAN ACGTCTCAG AAGACGACAG	420
GTGGGTGGTC NACNGCGCCC GATGGCCCGT ACGCGTGGGG TTAGTGCTTC NTCCAANAAC	480
ANAACCTCA TCNGACTACT GCGTCCCCAN CTCNCAATGG CCNTGCNCTG CAGGCAANAA	540
ATTCTACNGC CGAAGCCCCA TCCAAATCTC ATTCAACTAC AACTNNNGG CCNGCCNGGA	600
AAACCATCNG CTTCGGACTG CTTCAACAAC CCAAACTTGG TTGGCCACCN AACCCGAACC	660
ATCTCCTTCC AAAAANGGTN CTGTTGTTN TGGATNAATC CCCCNTCCC CCAANCCCC	720
TCCTTGCCNC AAANTTNATA ACCCGGGAAC TTGGACCCCC TCCAACCC	768

## (2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 764 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CACGANGAAA CGTCGTCGCC TACTGGCCCA GCGTCTCCTT TCGATACATA GCTGTCGGAA	60
ACGAGCTGAT CCCC GGATCG GATCTGGCGC AGTACATCCT CCCC GCCATG CGCAACATCT	120
ACAATGCTTT GTCCTCGGCT GGCCTGCAAA ACCAGATCAA GGTCTCGACC GCGGTCGACA	180
CGGGCGTCCT CGGCACGTCC TACCCTCCCT CCGCCGGCGC CTTCTCCTCC GCCGCCCAGG	240
CGTACCTGAG CCCCATCGTG CAGTTCTTGG CGAGTAACGG AGCGCCGCTC CTGGTCAATG	300
TGTACCCTTA TTTTAGCTAC ACCGGCAACC CGGGACAGAT CTCGCTGCCC TACGCCCTGT	360
TCACGGCCTC CGGCGTCGTC GTGCAGGATG GGC GATT CAN CTATCANAAA CCTGTTGAC	420
GCCATCGTCG ACGCGGTCTT CGCGGCGCTG GGANANAGTG GGAGGGGCGA ACGTGGCGGT	480
GGTGGTGT CN GAAAAGCGGG TGGCCGTCGG CGGGGCGGAN GAACCGAAGC GAGCACCAGC	540
AACGCGCAGA CGTTNCAACC AGA ACTTGAT CAGGCATGTT GGCGGANGAA CGCCNAAGAA	600
ACCANGGAAT GAAATCGAAG CTTACTTNNT CGAAATGTTT AACGAAAAAC CNCAAGGCTG	660
GAAGGATCCA ACANA ACTTT GGGCCTGTTT TATCCCAACA AAGCACCCGT CTACCAAATA	720
AGCTTCTAAA AACTA ACTT TGTTANGGTT GAAGAATCNT CNCC	764

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 764 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ACGANAGAAC CCTTTTGACA GAGTTGTTGT CATGGCAACA AAAGCTTCTC TCTCCATAAA	60
AGGCTTTGCC TTGCTGGTTT CAGTCCTTGT AGCAGTTCCA ACAAGAGTGC AATCGATTGG	120
TGTCTGCTAC GGCATGCTCG GCAACAATCT TCCCCGCCCG AGCGAGGTGG TCAGTCTCTA	180
CAAATCCAAC AACATCGCGA GGATGAGACT CTACGATCCA AACCAAGCCG CCCTGCAAGC	240
CCTCAGGAAC TCCAACATCC AAGTCTGTG GGATGTCCCC CGATCCGACG TGCAGTCACT	300
GGCCTCCAAT CCTTCGGCCG CCGGCGACTG GATCCGGAGG AACGTCGTCG CCTACTGGCC	360
CAGCGTCTCC TTTCGATACA TAGCTGTCGG AAACGAGCTG ATCCCCGGAT CGGATCTGGC	420

```

GCAGTACNTC CTCCCCGCCA TCGCAACAT CTACAATGCT TTGTCTCGG CTGGCCTGCA      180
AAACCAGATC AAGGTCTCGA CCGCGGTCTGA AACGGGCGTC CTCGGCACGT CCTACCCTCC      540
CTCCGCCGGC GCCTTCTCCT CCGCCGCCCA GCGGTNCCTG AGCCCCATCG TGCAGTTCTT      600
GGCGANTAAC GGANCGCCGC TCCTGGTCAA TGTGTACCCT TTATTTTAC CTACACCCGG      660
CAACCGGGAC AGATCTCGCT GCCCTACNCC CCTGTTACG GGCTCCGGCG TCNTCTTGCN      720
GGATGGGCGA NTCACTTTCA NAACTGTTT CNACNCCATC NTCA                          764

```

## (2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 806 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: U-36

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

ACGAGACCTT TTGACAGAGT TGTGTGTCATG GCAACAAAAG CTTCTCTCTC CATAAAAGGC      60
TTTGCCCTTGC TGGTTTCAGT CCTTGTAGCA GTTCCAACAA GAGTGCAATC GATTGGTGTC      120
TGCTACGGCA TGCTCGGCAA CAATCTTCCC CCGCCCAGCG AGGTGGTCAG TCTCTACAAA      180
TCCAACAACA TCGCGAGGAT GAGACTCTAC GATCCAAACC AAGCCGCCCT GCAAGCCCTC      240
AGGAACTCCA ACATCCAAGT CCTGTTGGAT GTCCCCGAT CCGACGTGCA GTCACTGGCC      300
TCCAATCCTT CGGCCGCCG CACTGGATC CGGAGGAACG TCGTCGCCTA CTGGCCCAGC      360
GTCTCCTTTC GATACATAGC TGTCGGAAAC GAGCTGATCC CCGGATCGGA TCTGGCGCAG      420
TACATCCTCC CCGCCATGCG CAACATCTAC AATGCTTTGT CCTCGGCTGG CCTGCAAAAC      480
CAGATCAAGG TCTCGACCGC GGTCGACACG GCGTCTCTCG GCACGTCCTA CCCTCCCTCC      540
GCCGGCGCCT TCTCTCCGC CGCCAGGCG TACCTGAGCC CCATCGTGCA GTTCTTGCGC      600
AATAACGGAN CGCCGCTCCT GGTCAATGTG TACCTTATTT TANCTACACC GGCAACCCGG      660
GANAGATCTC GCTGCCCTAC GCCCTGTTTC ACGGGCTCCG GCGTCTCCTT GCAGGATGGG      720
CNAATCANCT ATCAAACTG TTCGACNCCA TCNTCAANGC GGTCTCCCGG CGCTGGAAAA      780
AATGGGANGG GCAAACCTGC NGTGGT                                             806

```

## (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 726 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: U-53

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ACGAAGAAAN AANAGAACCT TTTGACAGAG TTGTTGTCAT GGCAACAAAA GCTTCTCTCT	60
CCATAAAAGG CTTTGCCTTG CTGGTTTCAG TCCTTGAGC AGTTCCAACA AGAGTGCAAT	120
CGATTGGTGT CTGCTACGGC ATGCTCGGCA ACAATCTTCC CCCGCCCAGC GAGGTGGTCA	180
GTCTCTACAA ATCCAACAAC ATCGCGAGGA TGAGACTCTA CGATCCAAAC CAAGCCGCCC	240
TGCAAGCCCT CAGGAACTCC AACATCCAAG TCCTGTTGGA TGTCCCCCGA TCCGACGTGC	300
AGTCACTGGC CTCCAATCCT TCGGCCGCGG GCGACTGGAT CCGGAGGAAA CGTCGTCGCC	360
TACTGGCCCA GCGTCTCCTT TCGATACATA GCTGTCGGAA AACGAAGCTG ATCCCCGGAT	420
CGGATCTGGC GCANTACATC CTCCCCGCCA TGCGCAACAT CTACAATGCT TTGTCTCGG	480
CTGGCCTGCA AAACCANATC AAGGTCTCNA CCGCGGTCGA CACGGGCGTC CTCNGCACNT	540
CCTACCCTCC CCTCCGCCGG CGNCTTNTCC TCCGCCGCC ANGNGTTNC CNTGAGCCCC	600
CNTCGTGCA TTTCTTGGG GANTTANCGG AGCCGCCNCT CCCTGGTTCA ATGTGTTTCC	660
CTTTATTTN NCCTACACCG GCCAACCCNG GGAACNAATT TCTNCTGCC CTANCGCCTT	720
GTTCCA	726

## (2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 810 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-58

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ACGANGNAAG AAGAGAACCT TTTGACAGAG TTGTTGTCAT GGCAACAAAA GCTTCTCTCT	60
CCATAAAAGG CTTTGCCTTG CTGGTTTCAG TCCTTGAGC AGTTCCAACA AGAGTGCAAT	120
CGATTGGTGT CTGCTACGGA ATGCTCGGCA ACAATCTTCC CCCGCCCAGC GAGGTGGTCA	180
GTCTCTACAA ATCCAACAAC ATCGCGAGGA TGAGACTCTA CGATCCAAAC CAGGCCGCCC	240
TGCAAGCCCT CAGGAACTCC AACATCCAAG TCCTGTTGGA TGTCCCCCGA TCCGACGTGC	300
AGTCACTGGC CTCCAATCCT TCGGCCGCGG GCGACTGGAT CCGGAGGAAC GTCGTCGCCT	360
ACTGGCCCAG CGTCTCCTTT CGATACATAG CTGTCGGAAA CGAGCTGATC CCCGGATCGG	420
ATCTGGCGCA GTACATCTC CCCGCCATGC GCAACATCTA CAATGCTTTG TCCTCGGCTG	480
GCCTGCAAAA CCAGATCAAG GTCTCGACCG CGGTCGACAC GGGCGTCCTC GGCACGTCTT	540
ACCTCCCTC CGCCGGCGCC TTCTCCTCCG CCGCCCAGGC GTTACTGAGC CCCATCGTGC	600
AGTTCTTGGC GANTAACGGA ACGCCGCTCC TGGTCAATGT GTACCCTTTA TTTTGTAGCTA	660
CACCGGCAAC CCGGGANAGA TCTCGCTGCC CTACNCCCTG TTCACGGGCT CCGGCGTCTT	720

CCTGCAGGAT GGGCGATCNN CTATCAAAC GTTCNACCCA TCGTCAANCC GTCTTCCCGG 780  
 CCTGGAAAAA TGGGAAGGGC AACTTGCNGT 810

## (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 710 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-72

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CACNAGTGGC CCAGCGTCTC CTTTCGATAC ATAGCTGTG GAAACGAGCT GATCCCCGGA 60  
 TCGGATCTGG CGCAGTACAT CCTCCCCGCC ATGCGCAACA TCTACAATGC TTTGTCTCTG 120  
 GCTGGCCTGC AAAACCAGAT CAAGGTCTCG ACCGCGGTG ACACGGGCGT CCTCGGCACG 180  
 TCCTACCCTC CCTCCGCCGG CGCCTTCTCC TCCGCCGCC AGGCGTACCT GAGCCCCATC 240  
 GTGCAGTTCT TGGCGAGTAA CGGAGCGCCG CTCCTGGTCA ATGTGTACCC TTATTTTAGC 300  
 TACACCGGCA ACCCGGGACA GATCTCGCTG CCCTACGCCC TGTTCACGGC CTCCGGCGTC 360  
 GTCGTGCAGG ATGGGCGATT CAGCTATCAG AACCTGTTG ACGCCATCGT CGACGCGGTC 420  
 TTCGCGGCGC TGGGAAAAAN TGGGAAGGGG CGAACGTGGC GGTGGTGGTG TTCNGAAAAA 480  
 CGGGTGGGCC GTCCGCGGGG CGGGAAGAAC CNAAANCGAN CACCANCAAC GCGCNAAACG 540  
 TTTCAACCAG AAACCTTGAT CAGGCATGTT GGCGGAAGGA ACGCCNAAGG AAACCANNNG 600  
 AAGGANATCN AGGCTTTCAT TTTCCAANAT TTCAACCAA AACCNANNGG TTGGAAGGAT 660  
 CNANCAAAA TTTTGGCCTG TTTNTCCCAA CAANCANCCC GTCTACCAA 710

## (2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 750 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-86

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CACGAGAGAG AACCTTTTG ACAGAGTTGT TGTCATGGCA ACAAAGCTT CTCTCTCCAT 60  
 AAAAGGCTTT GCCTTGCTGG TTTCACTCCT TGTAGCAGTT CCAACAAGAG TGCAATCGAT 120  
 TGGTGTCTGC TACGGAATGC TCGGCAACAA TCTTCCCCCG CCCAGCGAGG TGGTCAGTCT 180  
 CTACAAATCC AACACATCG CGAGGATGAG ACTCTACGAT CCAAACCAGG CCGCCCTGCA 240



AGCCCTCAGG AACTCCAACA TCCAAGTCCT GTTGGATGTC CCCCAGATCCG ACGTGCAGTC	300
ACTGGCCTCC AATCCTTCGG CCGCCGGCGA CTGGATCCGG AGGAACGTCG TCGCCTACTG	360
GCCCAGCGTC TCCTTTCGAT ACATAGCTGT CGGAAACGAG CTGATCCCCG GATCGGATCT	420
GGCGCAGTAC ATCCTCCCCG CCATGCGCAA CATCTACAAT GCTTTGTCCT CGGCTGGCCT	480
GCAAAACCAG ATCAAGGTCT CGACCGCGGT CGACACGGGC GTCCTCGGCA CGTCCTACCC	540
TCCCTCCGCC GGCGCCTTCT CCTCCGCCGC CCAAGCGTAC CTGANCCCCA TCGTGCAGTT	600
CTTTGGCGAN TAACGGAACG CCGCTCCTGG TCAATGTTGT TNCCTTATTT TTAGCTACNC	660
CGGCAACCCG GGANAGATCT CGCTGCCTAC NCCCTGTTCA CGGCTCCNGG CGTCTTCTGC	720
AGGATGGGCG ATCCNCCTCA AACTGTTCA	750

## (2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 745 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-96

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CACGAGGAAA CCCTTTTGAC AGAGTTGTTG TCATGGCAAC AAAAGCTTCT CTCTCCATAA	60
AAGGCCTTGC CTTGCTGGTT TCAGTCCTTG TAGCAGTTCC AACAAGAGTG CAATCGATTG	120
GTGTCTGCTA CGGAATGCTC GGCAACAATC TTCCCCCGCC CAGCGAGGTG GTCAGTCTCT	180
ACAAATCCAA CAACATCGCG AGGATGAGAC TCTACGATCC AAACCAGGCC GCCCTGCAAG	240
CCCTCAGGAA CTCCAACATC CAAGTCCTGT TGGATGTCCC CCGATCCGAC GTGCAGTCAC	300
TGGCCTCCAA TCCTTCGGCC GCCGGCGACT GGATCCGGAG GAAACGTCGT CGCCTACTGG	360
CCCAGCGTCT CCTTTCGATA CATAGCTGTC GGAAACGAGC TGATCCCCGG ATCGGATCTG	420
GCGCAGTACA TCCTCCCCGC CATGCGCAAC ATCTACAATG CTTTGTCCCTC GGCTGGCCTG	480
CAAAACCAGA TCAAGGTCTC GACCGCGGTC GANACGGGCG TCCTCGGCAC GTTCCTAACC	540
CCCCTCCGCC GGGGCCTTCT CCTCCGCCGC CCAAGCGTAC CTGAACCCCA TCGTGCAGTT	600
CTTGGGCGAA TAACGGAACG CCGCTCCCTG GTCNATGTGT NCCTTATTTA NCTACNCCGG	660
NAACCCNGGA NAGATCTCGC TGGCCTACGC CTGTTNCNGG GCTCCNGCGT CTCCTTGCA	720
GGAAGGGCAA TCACTATCAA AACTG	745

## (2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 749 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CACNAGAGAG AACCCCTTTG ACAGAGTTGT TGTCATGGCA ACAAAGCTT CTCTCTCCAT	60
AAAAGGCTTT GCCTTGCTGG TTTCAGTCCT TGTCAGTTC CCAACAAGAG TGCAATCGAT	120
TGGTGTCTGC TACGGCATGC TCGGCAACAA TCTTCCCCCG CCCAGCGAGG TGGTCAGTCT	180
CTACAAATCC AACAAATCG CGAGGATGAG ACTCTACGAT CCAAACCAAG CCGCCCTGCA	240
AGCCCTCAGG AACTCCAACA TCCAAGTCCT GTTGATGTC CCCCAGTCCG ACNTGCAGTC	300
ACTGGCCTCC AATCCTTCGG CCGCCGGCGA CTGGATCCGG AGGAAACGTC GTCGCCTACT	360
GGCCCAGCGT CTCCTTTCGA TACATAGCTG TCGGGAAACG AGCTGATCCC CGGGATCGGG	420
ATCTGGCGCA GTTACATCCT CCCCCGCCAT GCGCAACATC TACAATGCTT TGTCTCGGC	480
TGGCCTGCAA AACCAGATCA AGGTCTCGAC CGCGGTCGAC ACNGGCGTTC CTCGGCACGT	540
CCTANCCTCC CTCGCCGGG GCCTTCTCCT CCGCCGCCCA AGCGTNCTGA CCCCATCGTG	600
CAGTTCTTGG CGAATAACGG ANCGCCGCTC CTGGTCNATG TGTACCTTAT TTTANCTACA	660
CCGGCACCCN GGACAGATCC CGCTGCCCTA CGCCCTGTG CACGGGCTCC NGCGTTCTTC	720
NTTGAGGAT GGGCGANTCA CTATCANAA	749

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 648 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CACAAGGGAA GAAGAGAACC CTTTGACAG AGTTGTTGTC ATGGCAACAA AAGCTTCTCT	60
CTCCATAAAA GGCTTTGCCT TGCTGGTTTC AGTCCTTGTA GCAGTTCCAA CAAGAGTGCA	120
ATCGATTGGT GTCTGCTACG GCATGCTCGG CAACAATCTT CCCCCGCCA GCGAGGTGGT	180
CAGTCTCTAC AATCCAACA AATCGCGAGG ATGAGACTCT ACGATCCAAA CCAAGCCGCC	240
CTGCAAGCCC TCAGGAACTC CAACATCCAA GTCCTGTTGG ATGTCCCCCG ATNCAACGTG	300
CAGTCACTGG CCTCAATCC TTCGGCCGCC GCGACTGGA TCCGGAGGAA ACGTCGTCNC	360
CTACTGGCCC AGCGTCTCCT TTCGATACAT AGCTGTCGGA AAACGANCTG ATCCCCGGAT	420
CGGATCTGG CGCAGTTACA TCCTCCCCCG CCATGCGCAA CATCTACAAT GCTTGTCTCT	480
CGGCTGGCCT GCAAACACAG ATCNANGTCT CGACCGCGGG TCGACACGGG CGTCTCGGC	540
ACGTTCTTAC CCTCCCTCCG CCGGNGCCTT CTCCTCCGTC GCCCCANGCG TTCCTGANCC	600

CCCATCCGTG CAGTTCTTNG GGCNAATTAA CGGANCGCCG CTCCTGG

648

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 757 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CACGAGAAGA AGAGAACCTT TTGACAGAGT TGTTGTCATG GCAACAAAAG CTTCTCTCTC	60
CATAAAAGGC TTTGCCTTGC TGGTTTCAGT CTTGTAGCA GTTCCAACAA GAGTGCAATC	120
GATTGGTGTC TGCTACGGCA TGCTCGGCAA CAATCTTCCC CCGCCCAGCG AGGTGGTCAG	180
TCTCTACAAA TCCAACAACA TCGCGAGGAT GAGACTCTAC GATCCAAACC AAGCCGCCCT	240
GCAAGCCCTC AGGAACTCCA ACATCCAAGT CCTGTTGGAT GTCCCCGAT CCGACGTGCA	300
GTCACTGGCC TCCAATCCTT CGGCCGCCGG CGACTGGATC CGGAGGAAAC GTCGTCGCCT	360
ACTGGCCCAG CGTCTCCTTT CGATACATAG CTGTCGAAA CGAGCTGATC CCCGGGATCG	420
GATCTGGCGC AGTACATCCT CCCCGCCATG CGCAACATCT ACAATGCTTT GTCCTCGGCT	480
GGCCTGCAAA ACCAGATCAA GGTCTCGACC GCGGTCGAAA CGGGCGTCCT CGGCACGTCC	540
TACCTCCCTC CGCCGGCGCC TTCTCCTCCG CCGCCCAAGC GTNCTGANCC CCATCGTGCA	600
GTTCTTGGGC GAATAACGGA NCGCCGCTCC TGGGTCAATG TGTCCTTAT TTTANCTACA	660
CCGGCAACCC CGGGANAGAT TTCGCTGCCC TACCCCTTGT TCACGGGCTC CCGGCGTCNT	720
CTTGCAGGAT NGGGGGANTC CGCTATCAAA AACCTNT	757

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 748 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CACNAGCTTT TGACAGAGTT GTTGTATG CAACAAAAGC TTCTCTCTCC ATAAAAGGCT	60
TTGCCTTGCT GGTTCAGTC CTTGTAGCAG TTCCAACAAG AGTGCAATCG ATTGGTGTCT	120
GCTACGGAAT GCTCGGCAAC AATCTTCCCC CGCCCAGCGA GGTGGTCAGT CTCTACAAAT	180
CCAACAACAT CGCGAGGATG AGACTCTACG ATCCAACCA GGCCGCCCTG CAAGCCCTCA	240

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GGAACTCCAA CATCCAAGTC CTGTTGGATG TCCCCCGATC CGACGTGCAG TCACTGGCCT      300
CCAATCCTTC GGCCGCCGGC GACTGGATCC GGAGGAAACG TCGTCGCCTA CTGGCCCAGC      360
GTCTCCTTTC GATACATAGC TGTCGGAAAC GAGCTGATCC CCGGATCGGA TCTGGCGCAG      420
TACATCCTCC CCGCCATGCG CAACATCTAC AATGCTTTGT CCTCGGCTGG CCTGCAAAAC      480
CAGATCAAGG TCTCGACCGC GGTCGACACG GGCCTCCTCG GCACGTCCTA ACCTCCCTCC      540
GCCGGNGCCT TCTCCTCCGC CGCCCANGCG TTACCTGAGC CCCATCGTGC AGTTCTTGGC      600
GANTNNCGGA ACGCCGCTCC CTGGTCAATG TGTTACCTTT ATTTTAACTA CACCGGGCAA      660
CCCCGGGANA GATCTCGCTG GCCCTACCCC TGTTACGGC CTCCGGCGTT CNTCGTGCAG      720
GANGGGCGAN TCACTNTCAN AACCTGTC                                          748

```

## (2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 700 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-89

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

CACGAGGGCG GAGATGGGGA GCTGGCGGGC TCTGTTGCAG CGGCGGCTGC TGTGCTCTC      60
TGCTTTGGCG GTGGCTGTTC GTGTGAAGGC ACTCANCAGA GACNATTTCC CCGCCGGCTT      120
CATTTTGGC GCAGGCACCT CCGCTTATCA GGTAGAAGGT GCAGCTGCAG AGGGGGGAAG      180
AACACCCAGC ATTTGGGACA CGTTTACGCA TGCAGGGAGA ACTTTCGACC AGAGCACCGG      240
AGACGTAGCG GCTGATCAGT ATCACAAGTA CAAGGAAGAT GTGAAGCTGA TGCATGAGAT      300
GGGCTTCGAT GCTTACAGAT TCTCCATCTC CTGGTCCAGA GTTATCCCCA ATGGTCGAGG      360
GCCTGTGAAT CCACAAGGCT TCGGTACTA CAACAACCTG ATCGATGAGC TCAAAAGATN      420
TGGAATCGAG CCTCATGTCA CTCTTACCA CTTCGACCTT CCGCAAGCAC TGGAAGACGA      480
ATTACGCCGG GCAGCTGAAC CCAAAGATCG TANAAGACTT CACCGCTTAC NCCAACGTGT      540
GCTTCANCGA ATTTGGGGAT CNAATCNAGC ACTGGATCAC CGTCAATGAA CCAACATAN      600
ATTCCGTCCT CCGCCACCAT TTCCGCATCT TCCCCCTGG CCGCTGCTCT TATCCCTTCC      660
GCCTCCAACT TGCNCCAAGG GCACTCTCCC NTTGAACCAT                               700

```

## (2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 746 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: U-129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CACCGGAGAT GGGGAGCTGG CGGGCTCTGT TGCAGCGGCG GCTGCTGTTG CTCTCTGCTT	60
TGGCGGTGGC TGTTCTGTG AAGGCACTCA GCAGAGACGA TTTCCCCGCC GGCTTCATT	120
TTGGCGCAGG CACCTCCGCT TATCAGGTAG AAGGTGCAGC TGCAGAGGGG GGAAGAACAC	180
CCAGCATTTG GGACACATT ACGCATGCAG GGAGAACTCT CGACCAGAGC ACCGGAGACG	240
TAGCAGCTGA TCAGTATCAC AAGTACAAGG AAAGATGTGA AGCTGATGCA TGAGATGGGC	300
TTGATGCTT ACAGATTCTC CATCTCCTGG TCCAGAGTTA TCCCCAATGG TCGAGGGCCT	360
GTGAATCCAC AAGGGTTGCG GTACTACAAC AACCTGATCG ATGAGCTCAA AAGATATGGA	420
ATCGANCCTC ATGTCACTCT TTACCACTTC GACCTCCGC AAGCACTGGG AAGACNANTA	480
CNCCGGGCAN CTGAACCCAA AGATCNTANA AGACTTCACC GCTTACGCCA ACGTGTGCTT	540
CACGAATTTG GGGATCGANT CANCACTGGA TCACCCGTCN ATGAACCCAA CATANATCCC	600
GTCTCCGNC ACGATTTCCG CATCTTCGCG CCTGGCCGCT GCTCTTATCC CTTCCGNCTC	660
AACTGCNCCA AGGGCAACTC CCCCANTGAA CCATACATCG CCCACATAAC CTTCTGCTCT	720
CCATGCATCA CACCGCCTGT NCAAAA	746

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 798 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

ACGAGGTTCTG CCTCTCGCTT CTGTATCGTC TCGCGCTCGC TCGAAGCCTC TCGTTTCGTC	60
CGCCTCCCGG TCTCGATCCC CGATGGCGGA TCGAAGATC GCCAAGCTCC AATCCGCCGT	120
CGCTGAACTC AATCAGATCA GTGAAAATGA GAAATCTGGA TTTATCAGCC TAGTGTCTCG	180
CTATCTGAGT GGCGAGGCAG AACAGATCGA GTGGAGTAAG ATCCAGACTC CGACTGATGA	240
AGTGGTCGTG CCTTATGATA CCCTGTCACC ACCTCCGGAA GATCTTGAGG CAACCAAGAA	300
ACTTCTCGAC NAGCTTGCGG TGCTAAAGCT CAATGGAGGA CTGGGAACCA CCATGGGATG	360
CACGGGGCCT AAATCTGTTA TTGAAGTGCG TAATGGATTT ACATTCCTCG ATCTGATTGT	420
TATCCAAATA GAGTCTCTCA ATAAGAAGTA TGGATGCAAT GTCCCTCTGC TTTTGATGAA	480
TTCTTTCAAC ACTCATGATG ATACACAAAA GATCGTGGAG AAATATGCCA ACTCAAATAT	540
TGAGATTCAT ACATTTAACC AGAGCCAGTA CCTCGTTTGG TTATGGAAGA TTTCCAGCCA	600
CTGCCAAGCA AAGGCCNCGC CGGGAAGGAT GGCTGGTATC CCCAGTTCA TGGTGATTTT	660

TCCCATCCTT GATGAACAGT GGGCNAGCTT TGATGCCTTN CTATCACAGG GCAANGGAAT 720  
 NTGTCTTCNT TGCNAACTC GGATACTTGG GGTGNTNTNA NTTGAANTTA AAAATCCTAA 780  
 NCCATTTGAN TTNCNNCC 798

## (2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 788 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-26

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CACGAGGCAG AATTGTCTCC CACGCTGAGC AAGAGCATCT TTGAAGGAGC CGGTGGATCT 60  
 TACTCTACTT GGTCAAGTGC CGATCTCCCC CTTCTTACTG ATGCAAAGCT CGGCGGAGGC 120  
 AAGCTTGTCC TGAAACCACT GGGCTTGGCG TTGCCTCACT ATTCCGACTC ATCGAAAGTC 180  
 GGCTATGTTT TTGAAGGAAG AGCGGTGGTG GGGCTAACAC TCTATGGAGA GACCGAGCAG 240  
 AGGATACTGC TGCTTGAGAA GGGAGATGTG GTAGCGGTGG TCATGGGGAG CCTCACGTGG 300  
 TGGTACAACG AGGAGGAGGA CTCCGACTTC TCCATCGCCT TCTTAGGCGA TACCGCGACA 360  
 GCTGTGCGAC CGGGCGACAT CGCCTACTTC TTCTTGCGAG GATCCCTAGG AGTGCTCCAT 420  
 GGCTTTTTCGA CGGAAATTCC TCANCAGGGC CTGCGGTATA AGGGATGCGG AANCTGAGGA 480  
 AGCTCTTCGG AAGCCAACCT GGTACTCTAA TCATCACACT GCAGCAAAAG CTGCCTGGCC 540  
 TCAGANCATC CCGAGCTGAC TGCGAAGGGA TAGTCGTNAA CGCTGANCGC GTNNCGGCAT 600  
 ATATCAATGT GAAAANTGGT GGCTGTGCTG CGTCNGTGAA ACNTTGAATG AACTGGCNGC 660  
 NCTGGGAAGA TTCAGGTTCT CCGTCAACTC NCAANACTCN AACCTAACNC CNTTCGCTTG 720  
 CCGGGGTTCT TCCTTGATNC ACTGTNCANC TANTNTNTTT CCCNAAGGC NNTGGANCAA 780  
 TTCAAATC 788

## (2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 779 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ACGAGGCTTG TCCTGAAACC ACTGGGCTTG GCGTTGCCTC ACTATTCCGA CTCATCGAAA 60

GTCTGGCTATG TTCTTGAAGG AAGAGCGGTG GTGGGGCTAA CACTCTATGG AGAGACCGAG	120
CAGAGGATAC TGCTGCTTGA GAAGGGAGAT GTGGTAGCGG TGGTCATGGG GAGCCTCACG	180
TGGTGGTACA ACGAGGAGGA GGACTCCGAC TTCTCCATCG CCTTCTTAGG CGATACCGCG	240
ACAGCTGTGC GACCGGGCGA CATCGCCTAC TTCTTCTTGG CAGGATCCCT AGGAGTGCTC	300
CATGGCTTTT CGACGGAATT CCTCAGCAGG GCCTGCGGTA TAAGGGATGC GGAAGCTGAG	360
GAGCTCTTCG GAAGCCAACC TGGTACTCTA ATCATCACAC TGCAGCAAAA GCTGCCTGGC	420
CTCAGAGCAT CCCGAGCTGA CAGCGAAAGG GATAGTCGTA AACGCTGAGC GCGTANCGGC	480
ATATATCAAT GTGAAAAGTG GTGGCTGTGC TGCCTCGGTG ACACGTGATG AACTGGCGGC	540
GCTGGGANGA TTCAGTTTCT CCGTCGACCT CACAAGACTC GAGCCTAACG CCGTGCGCTT	600
GCCGGGGTTC TTCNTTGATG CAGCTGTGCA CTGATNTATG TCCCCAAAGG CAGTGGACNA	660
ATTCAGATCN CTGGCNCCGA TGGCAACCGT GCTTTTGGAT GCANAATTGA AGGAAGGGTT	720
TCTGTTTGGG CTCCCCAANT TCTTCNCGAT NACGGTCATA NCGGGCGCAA AGGGATGGA	779

## (2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 750 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-63

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CACGAGGTAA GAANGACAAG CGATGGCAGC AGAATTGTCT CCCACGCTGA GCAAGAGCAT	60
CTTTGAAGGA GCCGGTGGAT CTTACTCTAC TTGGTCAGGT GCCGATCTCC CCCTTCTTAC	120
TGATGCAAAG CTCGGCGGAG GCAAGCTTGT CCTGAAACCA CTGGGCTTGG CGTTGCCTCA	180
CTATTCCGAC TCATCGAAAG TCGGCTATGT TCTTGAAGGA AGAGCGGTGG TGGGGCTAAC	240
ACTCTATGGA GAGACCGAGC AGAGGATACT GCTGCTTGAG AAGGGAGATG TGGTATCGGT	300
GGTCATGGGG AGCCTCACGT GGTGGTACAA CGAGGAGGAG GACTCCGACT TCTCCATCGC	360
CTTCTTAGGC GATACCGCGA CAGCTGTGCG ACCGGGCGAC ATCGCCTACT TCTTCTTGGC	420
AGGGATCCCT ANGAGTGCTC CATGGCTTTT CGACGGAATT CCTCNCAGG GCCTGCGGTA	480
TAANGGATGC GGAAGCTGAA GANCTCTTCC CGAAGCCAAC CTGGTACTCT AATCATCACA	540
CTGCANCAAA AGCTGCCTGG CCTCANAACA TCCCGANCTG ACACCGAAGG GATATCNTAA	600
ACCCTGAACG CCGTTCNCGC ATATTTCAAT GTTNAAATT GTGGGTGTTG CTGCNTCCGG	660
TGACCCTTAT TAACTGGCCG GCGCCTGGGA AGAATCNGG TTCTCNTCC AACTCCCAAN	720
AATNCAAACC TACCCCTTG CNNTNCCGGG	750

## (2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 784 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-29

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

CACGAAGNAA AACTAGGTGA GAAGGAGATA ATCGTTGACC GAGGAGAGAA TGGCGAGCGA	60
GAAGAGCAAA ATCCTGATCA TCGGGGGCAC CGGGTACATC GGCAAGTTCA TCGTGTTTGC	120
GAGCGCCAGG TTAGGTAACC CTACCTTCGC TCTCGTCCGG AGCACCACCG CCCCCGCCGG	180
CCAACCCGAG AAGGCCAAGC TCCTGAGCGA CTTCCAGGCC GCCGGCGTCA CCCTCGTCCA	240
GGGGGATATA TATAACCACG AGAGTCTGGT TAAGGCGATC AAGCTGGTGG ATGTGGTCAT	300
CTCCCCCGTC GGCTTCGGGC AGCTGAGTGA TCAGACCAAG ATCATCGACG CCATCAAAGA	360
AGCCGGAGGA CACATCAAGA GGTACCTTCC ATCGGGAGTT TGGCAACGAC GTATACCGAA	420
NCCATGCTGT GGAAGCCAGC AAAGTCGACC TTTGTCGTCN AGCAACAAAT CACAAGGGCT	480
GTTGAGGCAT CGGGTATCCC TTACACCTTT GTATCTTCCA ACTTCTTCGG TGGGTATTTC	540
CTCCCGGTAT TAGGACTGGC AGGAGCCNCT GGTCTCTCCC ACGGACAANG TTGTCCTCTT	600
TAAGGTGACG GGAACACANA AANCCGATCT TTCTTCAATT GAAAAACNAN ATCGGGGACN	660
TTCACCATT TAAAGCCGTGG GATGATCCGA AAACCCTGAC CAAGGTTCTN TATTCTGAAA	720
ACTTNCGCC ACCNTCTTNT TTTCATTAAC AANCTCCTTT TCCNCCGGG GAAAAANAAG	780
GTCG	784

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 725 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: U-93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CACGAGGTGA GAAGGAGATA ATCGTTGACC GAGGAGAGAA TGGCGAGCGA GAAGAGCAAA	60
ATCCTGATCA TCGGGGGCAC CGGGTACATC GGCAAGTTCA TCGTGTTTGC GAGCGCCAGG	120
TTAGGTAACC CTACCTTCGC TCTCGTCCGG AGCACCACCG CCCCCGCCGG CCAACCCGAG	180
AAGGCCAAGC TCCTGAGCGA CTTCCAGGCC GCCGGCGTCA CCCTCGTCCA GGGGGATATA	240
TATAACCACG AGAGTCTGGT TAAGGCGATC AAGCTGGTGG ATGTGGTCAT CTCCCCCGTC	300
GGCTTCGGGC AGCTGAGTGA TCAGACCAAG ATCATCGACG CCATCAAAGA AGCCGGAGGA	360



CACATCAAGA GGTACCTTCC ATCGGAGTTT GGCAACGACG TNNACCGAAG CCATGCTGTC	420
GAGCCAGCAA AGTCGACCTT TGTCGTCAAG CAACAAATCA NAAGGGCTGT TGANGCATCN	480
GGTATCCCTT ACACCTTTGT TTCTTCCAAC TTCTTCGGTG GGTATTTCTT CCCGGTATTA	540
GGACAGGCAG GANCCACTGG TCCTCCCACG GACAANGTTG TCNTCTTAGG TGACGGGAAC	600
ACNAAAGCGA TCTTTCTCAA TGAAGACAAC TCCGGACTNC NCNATTAAAG CCAGTGGATG	660
ATCCGANAAC CCGAACAAGG TCTATATCTG AAAACTTCCG CCAACATCTT GTCTCTTAAC	720
AATC	725

## (2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 666 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-39

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

ACGAGCGCCA ACATGCTCAT CGCGTCGTGC GTCTCCGTCA CTCGCTCCCT CCCCACCCGG	60
CTCTCTTACG CCCCTCGCCA TCTCTGCCTC CTCGCCGCG CCTCCCCAA ACCCGTCCAG	120
AACAAATCCT TTCCTTGCCC TCTTTGGTCC GCCTCCTTCT CTTCTGCCT CGACCGCCGC	180
CCGAAATCCA CCACCTCCTC TGCCGCCCC CCGCCCTCTT CCATGGCCTT CGCTGCCGAC	240
AGCCTTGATT CGAACCCCTT CCTCCACGAC TTCGCCTTCC CCCCCTTCGA TGTGGTCGAG	300
CCGAAACACG TCCGCCCCGG GATCCGCGAG CTCTTGAGGA AACTCGAGAG CGATCTGGAG	360
AATCTGGANA GGACGGTGGA GCCGACATGG NCGAGGCTGG TGGTGCCGCT GGGAGAAAGA	420
TCATGGATTC GACTTCAGGT GGTCTGGGGA AATCCGTGAA CNATCTTGAA GTCCGTCAAG	480
GATTNCGCCC GGAAGTCCG ATCTGCTATC GAGGAAAGTC CCANCCAGAA AAAAGTTGAA	540
GTTTCAAGCT GAGGNTGGGA NAAAGTTAAG CCCTATANAT GATGCATTTT AANGNGAATT	600
CCNAAATTCT TCCCTCCATG GTCAANCCTT AAAGCGAAGG CCCCCTTAAC NTTTTATTGG	660
AAGCTC	666

## (2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 715 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-41

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ACGAGGTCGC CTCTCTCTTC AATTGCCTTC GAAGAGATCA GATCTGGTCT GATCAAGAAC	60
TCTCGATCGT GGGGAAGATG AGGGCGTGGT CGGCCGTCCT GCTGGTGGTC GCTGTAGCCT	120
TCGCGGCAGC GCGGAGGCG TCGAAGTCGA AGCCCAAGGT GTGCAACAAG GGGTGGGAGT	180
GCAGCGGCAG TATCTACTGC TGCAACGACA CCATCAGCGA CTAATTCAAG GTGTACCACT	240
TCGAGAACCT CTTACAGCAAG CGCAACTCCC CCGTGGCGCA CGCCGTCGGC TTCTGGGACT	300
ACCAGTCCTT CATCCTTGCC GCCTCCGTCT ACGAGCCTCT CGGGTTCGGC ACCACCGGCG	360
ACAAGGTGAC CAAGATGCAG GAGGTCCGCC CGCCTTCCTC CGGCCACGTT CGGCAAGCAA	420
GACCTCCCTG TTGGATATGG TGTTTGCCAC TGGTGGCCCA CTTGCATGGG GATTATGCTA	480
TAATCCATGA AAATGAACCC CAAGCCCAAG AATACTGTG ATCCCAAACCT ACCTTTATCC	540
CCTGTTTCCA ACGGAATTCC AATACTATGG ACGTTGGTGC TCTGCCTGTG TTAATTGGAA	600
ACTACAACCT ATGGGCTTCN TTGGCGAACC CCATNAAGGC AAATTTTGTT GAAACCATCC	660
CAAAATACCT TGGAAACAAA ATGCTACCCT TGGCTTTCCC AANCCGCTAT TTTGA	715

## (2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 654 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: U-57

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

ACGAGATTTT CTCTCTCTCT CTCTTCCTTC ACGGGCTTCT CGCTCCTCAT CTAGAGAAGT	60
GATCTGGGGC TTGGAGGCGG CTTTCTCGTA CTCCTCGCCT TGTTGGTTTA GAGATCATCT	120
ATAAATCTAT TCATATATAT TTTGACTCAG AGGGAGAAGG GGTTTTGGTA GATCGGTACT	180
GGAAATGTCT CGCTTGGAAG AGATGGCATC CATTGATGCC CACATGAGGC TTCTTGCCCC	240
CGGGAAGGTA TCCGAGGACG ACAAGCTGAT CGAGTATGAT GCCCTCCTCT TGGATCGGTT	300
CCTCGACATC CTTCAGGATC TCCACGGCGA GGAGATCAGA GAAACGGTTC AAGAATTATA	360
TGAGCTATCC TGCAGAATAT GAAGGCAATC CATGAACCTG AGAAGCCTAN AGGAAACTGG	420
GGAAATGTTC CTGACTAGTT TGGATCCAGG TTGACACAAT CCGTGGTCTC CCAAGTTCCA	480
TTCTCAGAC ATGCTTAACT TGGCCCAACT TGGCTGAAGA AGGTGCCAAA TGCTTATCCN	540
AANACGGATT CAAGCCTTAA AAAAAGGANA TTTTGTGAT GAAAATCCTG CCAATTACTT	600
GAATCCNGAC ATTAAAAAAA ACCTTTANCT TTCTTGTTGC NNCNCCTTAA AAAA	654

## (2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 790 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: U-109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ACGAGAGAGC ACAGGCCATG GCATCCACGG AGACGAGTAC TACGTCTACC ACCAACGACT	60
TCTCCGGCGG CAAGACCGCC CCGGAGTACG GATACGCGGT GCCGTCGCGG CCGCCTCCCA	120
ATCTCTTCTT CCTCGACTTC GGGCTGAGGC TCCTCCTCTT TGCGTCCGCC GTCACGGCGC	180
TCGTGGTCAT GGTCAACAGC AAGCAGACCA AACTTATTC CGTCACTGTG GCGCCTTCGT	240
CCCAGATCTT GGTCACTCGC GACGCCAAGT TTCAGCACTC TCCGGCCTTC ATATATCTGG	300
TGGCTGCGCT TTCGGTCACT GGTGTGTACA GCATCATCAC CATGTTGGTT TCCTTGTTTT	360
CTATCGCAAG CCCCTCTCCA TCACCAAAGA CGCTGTTCTT TCTCATCCTC CTTCCGACAC	420
GCTGATGGCC GGAGTGGATG GCTTCAGCCA CCGGGCAACG CGGGATCCGT CGCCCTACAT	480
AGGTCTTGAA AGGGCAACTC TCATGCGAAT TGGAAACAAG ATCTGCAACA TGTATGGGA	540
AAGTTCTGCC GGCACGTAA GCGGNTCCAC GGGCCGTCTC CCTCATCGCC TCCATCCGTC	600
CTCCGTCTTG CTCGTCNTGC TCTCCTCCCT ATCTCTCTAC CGTCGCANTC GCTAATGAAA	660
ANTTAAGCTT CACCTTCTCT CTTTACAGGT AAATTTGGGG TCNCTTTTAA TGGTGTTTTA	720
TCCANTCNCT GTCTGTGTCC CGTCTCTCNT TCGTCTTGTT NTTATGGTGA AATGTTGGTT	780
GCTCCNCCTT	790

(2) INFORMATION FOR SEQ ID NO: 52:

(i) .SEQUENCE CHARACTERISTICS:

(A) LENGTH: 784 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: U-134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

ACNAGCTTTG CGCTGCCCCC AGCGAAGAAG CCCAATTTC AGATCTCGCC ATGAAACGGG	60
GAAAAATCGA AGGTGATGC CCCAAGAAG GCCGACACCA AGCTGTCGGT GAAGAAGGGA	120
CCGGAGAGGG CGAGTAAGAA NCCGAGGAAG ACAAAGGCGG ACAAGGATCC GAACAAGCCC	180
AAGAGGCCTC CCAGCGCCTT CTTCTCTTC ATGGAAGAAT TCAGGAAGTC ATTCAAGGAA	240
AAGAATCCAA ATAACAAATC GGTCTCTGTG GTGGGTAAAG CCGGTGGAGA CAANTGGAAA	300
TCCTTGTCGG AAGCTGAGAA GGCTCCTTAT GTGGCCAAGG CAGCCAAGTT CAAGACAGAG	360
TACACCAAGA AAAATAGCTG CATAACAATA GAATCAGTCT GGGGGAGGAA GTCACGCTGC	420

TGCGGATGAA GATGAGTCCG ACAAGTCCAA GTCTGAGGTT GAACGATGAC GACNAANGAA	480
AGAAANANGG AAGCGAAGGA NGAAACANGA ANACNATGAA TGAGGAAAAC TGGAAGCAAG	540
TCTTGCTATG TTTATCTTTG TCTTCTTTCC CCCATCTTTG TTCTACCTTC TATGTTGAAT	600
GACAAAGCCN TGTTCCCTGAC CTGGCTGTTT GTCNCTAACG TTTTACTTTA CTTTTCCTCC	660
TAATTCCAAG CTTAATTAA TTGCCNAAA AAAAAAAAAA AAAAAAACC CTGGAAACCN	720
ATTGNCNGAA NCTGGGATCA NTCCTCCCTA CCAATACNTT TCCTTACTNT NATCANTGCT	780
TTGA	784

## (2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 729 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: U-37

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ACGAGCGAAA TCATGTCTTG ATAGAACCCG ACTTGCACTA TCAAGCAAGG CAGAATATTA	60
CCATCNAAAT TTTACAACCT TCAGCTGAAT ACCTTGGATC ATTGCTTGGT GTTGAACCGT	120
GGGCAGCAAG CATATTTACT GAAGAAATTA TTCGTGCTGG ATCGGCTGCT TCTTTATCAG	180
CACTTCTTAA TCGACTTGAC CCTGTCCTTC GGAAAGTGGC ACATCTAGGA AGTTGGCAGG	240
TCATAAGCCC TGTGGAAGTT ACTGGATATG TTGATGTCGT ANATGAATTG CTTGCTGTTC	300
AGAATAAATC TTACACACGG CCAACAATTT TGGTTGCAAA AAGTGTAAG GGAGAGGAGG	360
AAATACCAGA TGGCACAGTG GCCCGTGTTC AACACCTGAT ATGCCAGATG TTCCTATCTC	420
CATGTCTCCT GTTGCCGAAC CTAGAAAATA AGCAAGGGTC CTGCTTTTGC TACATGCTTT	480
GATGCCCAAT ATCCTGGCTG AAATTTCCAG AANAAATGAA AGGGAAACT GTTCCNGCT	540
ACAGCCCCAC ATCTGCTGAT ATAGTTGTTA TAGTTGAGAA TAAACNAGAA TTGAACTTGA	600
AGAATATCCA GTTCCGCCTA AAAATGGACA TGATCATCCN CCCCCACCTG TTGACTTTTG	660
GTCCCGGAAA CATTTTAATN GGTTAAAANT GCCNATNTCC NCNGACAAAT TCCCCCNTG	720
AAACGGGTG	729

## (2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 662 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: U-42

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

ACGAGGGCTA ACTAATTGAA TGCACTGTGT GTGTGTGTGA GAGAGAGAGA NAGANAGAGA      60
AGAGGAGAAA GAAAAGAGAA GTGGAATCAG ATACCATGAC ATCCTATATA GTCGACACCA      120
GCATTCTTTT CGCCCGTCAG CGGGCCATTT TATCATTGGT AAATAAGAAG ACTGCCGAGG      180
GTTGCATCGC TTCGTCTTCA TCGCGTTCCT CAACAAGGTG CGGGTCGAGG AGGAGGAGCA      240
TCGTCGAGTG CTCGAGCTCG GGCTGGAGCT GGAGCTGGAG CTGGANCTGG ATCTGGAGAG      300
GTGGGCGATC GGATAANCCG ACGATGGACC AAGGGAAAGG GTTCCGAGGG ATATGGTGCG      360
GCCGGGGCGA TGGTCTTCCG AGCCCGATTG TCCGAGGAGG GGGTCCTTTC CGGTTCGGAT      420
TGCTCCCNAG ACCCNACAGA NCTGCGGCGT TTCCTANCCT CTCCTTCCCG GATCCCTAAT      480
GTCAGGGANG CTCCCATCGC GGTTCGGTCC GGGTCCCCCG AATTACTTCC CCCCCTTCCG      540
ANCGTCCTCC GTGGCCANCA AAATNGTCCC GATCCAGTTT CCTTCCTGGG AAATCCCTTT      600
TTNTGGAACC CNGAAAANTC CTCCGGCNGC TTTGAACNGA CNNGAAATCC GGATTTTTTN      660
CC                                                                                   662

```

## (2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 711 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: U-47

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

ACGAGCGTCG TCGAGCGCTA CCCACGGGC GTCGCCGTTA TTACCATCAA TCGCCCCAGC      60
TCTCTCAACT CGCTCACACG CCCGATGATG GTATTGCTCG CCGCCGCCAT CAGGCGGCTC      120
GACGCCGACC CGGCGGTGGG CGCGCTGGTG ATCACCGGGA GGGGCCGGGC CTTCTGCTCC      180
GGCGTCGATC TCACGGCCGC CGAGGAGGTG TTCAAGGGCG ATGTCAAGGA CGTGGACGCC      240
AACCCCGTGG CCCANATGGA GCGCTGCCGC AAGCCCATAA TCGGGGCGGT GAACGGCTTC      300
GCCGTTACCG CCGGTTTCGA NATCGCCCTC CGCCTGCGAC ATCCTCCGTC GCCGGAAGG      360
ACGCCCAAGT TCATTGACAC CCACACCCAG GTTTTGAAT ATTTCCCATC CGTTGGGGCC      420
CTTTCACAAA AGCTCCCTCC GCATTATCCG GAAATAAGTT AGAACCACGA AANGTTATCA      480
CTTTCTTGGC ATGGCTATAA CTTGCCAAAA ATGGCAGAAA AGTGGGGCCT CCTCNACCAT      540
TTTGTGGGAA AATGGTGAAG TCTTTAAANA AAACCAAAAA AATTGCCCCT TGGCCATTTT      600
AAAAAACAAC AGGAAATGGT GTTTGAANTT TCAATTCNTC CTCCATGAAG GTTCCAATT      660
GGATTTTGGG TTCTTGCTCC TTGCCCTTG AAAAAGANAA AACTNCCCTT C                    711

```

## (2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 745 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

ACGAGTTCTC CTCCGTCTCT CGATTCTCCC CCACCGTTTC CCGATGTTGC TCGTTCGCTG      60
GAAGCCGGTC CTCCACTGCC CTCCCCAGGG GCACCGTCGC CGCGGATTCG CATGGCCTCG      120
AGGTCCGCGG CGATCACTGC TCCTCCGGCG CCCGATTCGC TCCCCGGCGC CTGCCTTCCT      180
ATCCATCTCC AGCTCTAAAT TCTCTCAGGC GGGTCGGGCG CGCGTCCGCC CCGTCGTTTC      240
GGCTGGTTTG GCCCAGACCC CGTCCCTCGC CGACGTCGAG AACNCCGAGA TCCTGTTCTC      300
GGAGACCCTC TCCTTGAAGC GGTCTCAGAC GGTGGAGGGG AAGATAACGG TGAGATTGGA      360
TCCAGCAGTC GCCCAGAGGAG GAAGTTGTCC AAATGGCGGT TGACCATCCG GTTGTAATTT      420
GGAAGGGGAA AGTTGGACTC CTGCACTGGG GAATTTAGCT ACTGCGAATG ATCTTGGAAG      480
GCGAAATGGG ATCAACCTCC TCCCTGAAAA TGAAACACC CCGAATTCTG TCCCTTAATT      540
AAAGGAATAA TGCCAATANA AACACCTTTT TGAAAAAAA TTATCATCCC CNATCCCGAA      600
AAGGCAAGCA CTTCCNCAAA ACTGCAAATT CGAAATTTTG AAANAGCNAC ACCCCCAAAT      660
TGGCAGCCAA TTCCATTTT GTTTTTTAA NGGAAAAAAA NAAAACCNGG ANCCNTTGGT      720
TTTCNGCCN CCAAGGGGAA AGGGA                                     745

```

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 728 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

ACGAGCGCAA TCTGGAATCC CCCGTTTCGCT TCCGCTTGCT GCCATTTCTT GTACGCACAC      60
GGAATCAGAT CTCGGACGTA TACCAACACG AAGAAGCAGA GAGGCGAGCC GGAATAAGTC      120
GATTAATCAG AGAAGAGAAC GAAGAAGGAT TCCTCGCCAT CCCCTAGGGT TTCGCCGATG      180
GCCAGCGCTG GCGGCGGCGT GGCGAGAGGG GGCCGGTTGG TTGGGGACTA TATGATCGGG      240
CAGCAGATCG GGGCTGGGGC GTTCTCCACT GTATGGCGGG CGCGACACCG CGTGCGGGGT      300
ACGGAGGTGG CCGTCAAGGA GATCGCCATG GACCGCCTCT CCAATAAGTT GCAGGAAAAC      360

```

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CTTCTGTCCG AGGTCTTCAT CCTCCCGTCC GCATCAACCA CCGCCAACAT CNTCCGCCCC      420
TTTACGACTT CCNTCCCANa ACTCCTGGCA GAAATATATC TCATATTGGA ATACTGCANA      480
AGTTGGCGAN TTGTCTGTGT TATATACANA ATCCATGGTA AAATTCCCAA AAACAACTGC      540
NAANCATTTT CTTGAAAACA AACTAACTTC CTGGTTTTGC AGTTCCTCCC CTTGAAAAC      600
AATNTTCTTT CCATCCTTGA CTTTAAAACC CNCAAAATCT TCCTTCCTCT NCATCNNTAT      660
NGGTTGAAAA TGCCTNTCCC CTGAAAATT TGCAAAACNTT NGGCTTTTNC AAATTTTCTG      720
CCCCCCCC                                         728

```

## (2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 763 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: U-66

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

ACNAGGNAAA AGTTCATAAA CCAGTTGTTG CTTGGGTTAG CGGAACCTGT GCACGCCTAT      60
TCAAATCAGA AGTGCAATTT GGTGCTGCTG GTGCAAAAAG TGGTGGCGAG TTGGAATCAG      120
CACAAGCGAA AAATCAGGCT CTAAGAAGAG CTGGAGCAGT TGTTCCCACT TCGTATGAAG      180
CATTTGAGAC TGCAATCAAA GAAACTTTTG AGAAACTGGT TGAAGAAGGG AAGATTGCTC      240
CTGTATCTGA AGTTAAACCT CCTCAAATTC CTGAGGATCT GAAATCTGCA ATCAAAAGTG      300
GGAAAGTCCG GGCTCCCACT CATATTATCT CCACTATTTC AGATGATAGA GGTGAAGAAC      360
CATGTTATGC TGGTGTAACCT ATGTCTACCA TTATCCAGCA TGGTTATGGT GTGGGTGATG      420
TAATTTCTCT TTTATGGTTC AAGCCGTAGT CTTCCACGTT ATTGCACACA ATTCATTGAG      480
ATCTGCATCA TGTTATGTTG CTGATCATGG TCCTTGTTGT TCTGGTGCTC ATAACACTAT      540
AGTTACGGCA AGANCTGGAA AGGATTTAGT TTCAAGTTTG GTCTCAGGGT TTGCTCACAA      600
TTGGTCCTCG ATTGGTGGT GCAATTGACA AAGCTGCTCC NATACTTTAA AGANGCATGT      660
GACAAAGGCT CACTCCATAT GAATCCGTGA AGGTTTGAAA AAAAAAGGAA TCCTGTTCNN      720
NGAANTAGGG CCCAGGATCC ANAATTNAAA ACNACNGGGA CCA                                         763

```

## (2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 764 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: U-84

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

ACGAGCAGCG GCGGTCTCGG CGGAAGAAGG CCTTCCGCAC CTGAGCTCGC AGGCCTACTT	60
GGAAGGCAAA GCCGTGGGGG AGTCCCGCGC CCTGGTGC GC	120
CAACCTCGGA TGGGTGACCG GAACCGGCGG CAGCATCACC GTCAAGGTCC ACGACGACGC	180
CGTCCCCAAG CCCCAACAGC TAATCGTCAT GTCCCCCTCG GGGGTTCAGA AGGAGCGGAT	240
GATGCCTGAG GATATGTACG TGTTGACTGG GAGTGGGGCC GTGCTATCTG CGCCGTCGCA	300
NAAGCCCTAC CCCATAAGC TTCCCAAGTG CACCGATTGT GCCCCCTCT TCATGAAGGC	360
TTATCANATG CGTAATGCTG GGGCTGTTAT TCATAGTCAT GGAATGGAAT CTTGTCTTAT	420
AACAATGCTT CATCCTTTCT CAAAGGAATT CAGGATAACT CCATATGGAG ATGATAAAAG	480
GAATTCAAGG GCATGTTTAT TATGATGAAT TGGTTATTCC CAATAATTGA AAAACACAGC	540
ACACGAACCT TGAACCTACT TGAATCCCTG AATCNACGAA TGGCAGCATA CCCNAAANCA	600
ATGCTGTGCT TGTGCCGAAC CATGGGATAT ACTTTTGGGG GAAAATCCTG GATAAATGCC	660
NAAANACAGG CTGAATTGCN ATCNTTATCT TTTTGAATG CTGCCCTTNA ACTCCCCTCC	720
ATTTAGTTTT GAATACNNTA ATCCAATTCN TGGTCCTGAA AAGG	764

## (2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 605 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-96

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACNAGGAAAA GCCCTCGGCC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC CTTGGAATCG	60
GAAGGAGAGA ANAAGAANA AGCGGAGAGT TCATGATGGC GCTTCCCGAN GAGAACGCGG	120
GCGAGGCGGC GCCTGATGCG ATGGCGGCGG CAGAGGAANA GACGGTCGCG GCGGTCGAAT	180
CGGTGCGAGA GGAGACCTCG GGGAAGACTG GCGGAGACCG ACCCATCTCG ACCATCCTGA	240
TCGTCAATTGC GATGCANACG GAGGCACTCC CTTTGGTGC CAAGTTCGGT CTCGCCGAGG	300
ATGCTGATGG ATCCGTGTTT CCTAAAGGTT TTCCATGGGT CANATACCAT GTTACCTACA	360
GAGGCCTGCA TATTGATCTA GTATGGCCAG GGNAAANATA TNNTATTTGG GTGTTGATAG	420
CGTTGGCACA GTNTCGTCAG CTCTTTTGAC GTTTGCTTCA ATTCNGGCCA TTGAAAACCA	480
NATCTTTATC NTCAATGCNG GAACCCGCCT GGTGGCTTTT ANTNNCAAAA GGANCATGCN	540
TTTAGGGGAT GTTCTACCTT CCCCTCTCCN TGTTGCTTTC CTTGANAGAA AGANTACCTT	600
ATTCC	605

## (2) INFORMATION FOR SEQ ID NO: 61:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 736 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

ACGAGCTCGA TCTTAGCGCG CCCCACTCGT TGGGAACCAC CATCATCGGA GTGACCTACG	60
ACGGCGGTGT CGTCCTCGGA GCCGATTCGA GGACGAGCAC AGGAATGTAT GTCGCTAATC	120
GGGCGTCGGA TAAGATCACA CAGTTGACGG ACAATGTCTA CATATGCCGC TCTGGATCGG	180
CAGCTGATTC CCAGTTATC TCTGACTATG TCAGATACTT TCTTCATCAA CACACAATTC	240
AGCTTGACA GCCTTCAACG GTCAAGGTGG CAGCTAATTT AGTTAGATTG CTGTCATACC	300
AAAACAAGAA CATGTACAA ATGGGCATCA TTGTTGGTGG ATGGGACAAA TACGAAGGAG	360
GTCAATATA TTCCGTGCCA CTTGGAGGGA CAATACTGAA GCAACCTTTT GCTATCGGAN	420
GATCTGGTTC CAGCTACCTT TATGGTTTCT TTGATCAAGC ATGGAAGGAA GGGATGAACC	480
AAGATGAAGC TGAATAAATT ANTGGTGAAN GCAGTCTCTC TTGCTATTGC ACCTTTATGG	540
GGCGAACGGA AGTGTCTCTC CGTACTGTTA CTATCAATGC TGAANGTGT CCCTTTATGG	600
TCTACTCCNG GGANCCCTTC CCCCTATGGC ATGAAACTG GACCCCCCAC TCCCTGCTGG	660
ATATCTCCNC TCCCACAATC CCCAACCTAT AACACATGAA NTCCTGGTCN CTGTTGCCAC	720
CCCCATCCCC NGNTTT	736

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 742 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

ACGAGGAGAA CCGAAGACGA GAAAGAATTC CACCAATCTC TCTCTACAGA TGGGTCGAGC	60
CGTTCTCTCT TCCTCTCTCG TCTCCCTGAG ACCAAGGATT CCCGCGGTAC CCAATCCTTT	120
TTTACCCAAT TCGACGCCCA ACAACGCCCT GCGGTTTCCC TCGAAGATTT CGCGGGGATC	180
CCGAACCCGC GCGGCGGCGG TCTCCGAATC CCCACCGGG AGGTTGTTCC CGAGGGTTGC	240
GGCCGANTCC ACGGGGCCGA TCCCCGCGGC GGAGCTGCTG AAGGTCNTGG AGACGGCTGC	300
GAGGACCGGC GCCGAGACAG GAGATTATGG TAAATGTAA GGTTTGCTGC AATGAGCATA	360

GACCATCGTT CTCTTAGCAA GAAAGATACA AAAAGGGGGC CAAAATAAGG TTGTGATGGA	420
AGCTGTTAAT AANCCTCGCA ACATTAATTA CNAAGGAAAT CACAGATTG GTGACGGAGT	480
TAAGANAAAT TAGTTATACG CTGTGCTACA TNATGGTGAA AGAATCACTG ATAAATTGAG	540
TGAATCAGTA ATTCTGGAAG TTATTGAAAA AGAACTTTAA AGATCATCTT ATACTTGGTG	600
AAGAANGTGG NCTTATTGGG GATTNNTTGT TCAAANTTTC TCTGGTTGCC TTGATCCNTT	660
TAAATGGAA CAACCAACCT TTGCTCCATG GTTCCCCAA CCTTCTNTT TTCCNTTGA	720
AATNTGTTT CCNTTNGAAA AC	742

## (2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 804 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: U-112

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACGAGGACGA GCAGAGGAGG CCGAATCTTG TTAGGGTTTC GTCCCCCTCCC TCTATCTCTC	60
TCTCTCATTA TCTTATCAGA GAAGCACACG AAGTAGACTG CGGAGATTGA CAGCAGGGAC	120
ATAAAGATGA AAGCTTGCTG TTGAATGCAC TCAGAGCCGA TGTGATTGAG GCCTTTCGAG	180
CAGCTGCATC TGTTCTTGAG GTCGTAAGTT TGCGCTTTTG AAGCTGTGGG TATCAAGTGA	240
TTGAGAGTA TTCTCCCCTG CGTTGAGGAT TGTCGAGGGC TTTAAACTTG TGTGGTGGA	300
TCGCAGCAGA TCGAAAGGTT CTGCCCCTGT TCCAGTCTCT TTCTGTTGGA TTGGTGCTTC	360
CGGGTGCTAT GAGCATGGCA GCAGATCATA ACATCAACTT CCCTCTTGA GGAGTTTTC	420
CACAATCTTT TTGCAATCAA CATGTTAGTT TCCTTTCCT CAGGGACTGT AAACAACACA	480
CACGGTATTT TCCCCGGTGG AAATGAACAT TTCAGGTGGA ATAAATGGAA CGACGGCGAA	540
TGATNTTGGC TGGAAATTCC CGGCACGCCT GAAACAATAT TTCTCCCTTT GGTATCGACT	600
ACTAATTCTC CCCGGAAATA TCCCCTCCGA ACCCACAACA TGGGCGTTNA GCCATCCNTA	660
CATCCATCCC TGTNGATTGG TCCTGCGAAG AATTTGGAAN TGANTGAAAC GAAGGCCTTG	720
CCNCATATGC TGGTGANCCC TAATATCCTG AAATTTTTTC CANATTGCTT CNTAACCTCC	780
CCTGACAAAA TTGTGAAGGA AGTT	804

## (2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 672 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:

(B) CLONE: D-24

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

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ACGAGCAAAA CCGCCGCTTT CGGCCCCCTT CACTTCTGCC ACTACTAGTA TGTGAGTACC      60
CGTCTCCGTC GCCGCAGCGG ATCGTTGATG GCGGATATCC CCTTGGCCGG GCTTCTCGAC      120
CTCCGCCTTT CCCCCGCCTC CTTCAAGGTC TCCCTCCAG GTCCGCCGCC CCTCCCCCTC      180
CGCCGCTCCT TCTCCGGGCC TCCGCCGGCC CCGACGACGA CGAGGTCCAA GGTGTTTCG      240
CAGGCCCTAT CGCGATCCAC TATGGAGCTC TTCTCCACCA CCGAGTGCTC CGACGGCAGC      300
GTCATCTTCC GTTTTGGTGA TCGACCGAA GCGAANAGGG ACGAGTTGC TGATGTTGCT      360
CCTTCTGAAA GCACCGGTTT CTGGAANAAA GATTTGGAAA ACGTTGGGA AATCCGGAAG      420
CNAAGATTC CCNAGGAAGA AAGGTCCTT GTTGANATAA ACCAACAAAA AGCTTGAAAA      480
GATACCATCT TTGAAAATGA ANGAAATCNN AATCCGTGG TGATAGGTTG AAGTAAGAAT      540
ATGAACGGGT GGTCCGTTTT CCGANATTAA AAATTCTGGG AATGGTTGA AACANATTCTN      600
AAATATTGAA TGAACGGATT TGTTTTGAAA GGANAATTGT NTATCCCTT CTNANTNAAA      660
ACNAATTATT GC
                                                                                   672

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## (2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 635 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: D-28

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

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GGANAATTGT NTATCCCTT CTNANTNAAA ACNAATTATT GCDNTTTCG GNCCTCGTTC      60
GCCTGCTTGT CGACACTAGT GGATCCAANC CAATTCGGCA CGAGCTTTT TTGCCGTTTC      120
CTTCTCTCAC GATGGTCCTC CACGACGCGG CGGCCGCGC GGATGCCGCC GAATCGGACG      180
CGGGTNNGGG GGAGGAGAAT AANATGCGGA NAAGGAATCN GAAGGGGCGG GGGATGAGGA      240
ACAACGCNAC NGCCCAATAN ATCCTTGCTT CCGGATTCTT CCGACNGTGG GCCTTCCCTG      300
ATGCCTCTGT CAACGACCTC CACNGACATN GCGATTACNG GANNCCCACC NGATCCNCGG      360
GACGGGTGGT GTTNTANTTC CACTCACACT CCACTTGTCT TNACGGGTTC TTGTCCCCNA      420
CNGCNCCTGGT GGAGANAGNN CTCNTNACAG GGGTGGATGT NCTNNCTNTN ACCCCACCCN      480
TCACTCCCTT NNCTGGNTGT TTCCNCAAGC CNGTTTGACA CCCTNCCNCT CTCTTCTTGN      540
CNNNTTNTCG GATTCATTCC CNCTCAATTT TTAACATTCC NTTCCCCCTT TNTNNTTCN      600
NCCCTCCGN GAACCTAANT CNTTNAATNT CCCNA
                                                                                   635

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## (2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 786 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: D-86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

ACGAGCTCTC TCGTTCGCCT CTCCCTCTCG TGCGATCCTC TCTCGGTTGC AGACTTTGTC	60
GGAGTAGTCG TGTTTGTTTT GAGTCCTAAT CACCATGGGG AAAGAGAAGG TTCACATCAG	120
CATTGTGGTC ATTGGCCATG TTGACTCCGG CAAGTCGACC ACCACCGGCC ATCTCATCTA	180
CAAGCTGGGT GGTATTGACA AGCGTGTGAT CGAGAGGTTT GAAAAGGAGG CTGCAGAAAT	240
GAACAAGAGG TCATTCAAGT ATGCCTGGGT TCTGGACAAG CTTAAGGCCG AGCGTGAGAG	300
AGGGATTACC ATTGATATTG CTCTTTGGAA GTTTGAGACC ACCAAGTACT ACTGCACTGT	360
GATTGACGCT CCCGGACATC GTGATTTTAT CAAGAACATG ATCACTGGAA CCTCCCAGGC	420
TGACTGTGCT GTTCTCATCA TTGATTCCGA CCACTGGTGG TTTCGAAGCT GGTATCTCTA	480
AGGATGGCCA GACTCCGTTG AGCATGCTCT GCTTGCTTTT ACTCTTGGGA GTCAAACAGA	540
TGATTTGCTG CTGCAACAAG ATGGACGCAA CCACCCCAAG TTTTCCAAGG CCANGTTATG	600
ATGAAATCCN TGAAAGGAAG TTCCTCCTTA CCTCCAGAAG GTCCGATATA ACCCTNAAAA	660
ANAAACCTTT CCTTCCTATC TCCTGGATTC CAAGGTTGAC ACNTGATTGA NAGTCNACAA	720
CTGGACTGGG TNCNAGGGCC NCTCTTCCTT GAANCCCCCA CTGATTCNNG AACCNAAGG	780
CCNCNA	786

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 712 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: D-38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

ACGAGATTTG CTTCAATTC CCGTTTCCTC TGACATCTTG CTTCGTAGTT TGATTTCTTC	60
TTAGTTCGAT TTCTTCTTAG TTCGATCGAT AGAGAGCATG GCGGGGAAAG GCGAGGGTCC	120
GGCGATCGGG ATCGATCTGG GGACGACGTA CTCGTGCGTC GGAGTATGGC AGCAGGACCG	180
GGTGGAGATC ATCGCCAACG ACCAGGGGAA ACCGCACCAC CCCCTCCTAC GTCGCTTTCA	240
CGGACACCGA GCGCCTCATC GGTGACGCCG CCAANAACCA GGTGGCCATG AACCCAATCA	300

ACACCGTCTT TGATGCAAAG CGTTTGATTG GGAGGCGATA CAGTGACTCT TCCGTCCAGA	360
GTGACATAAA ACTATGGCCG TTCAAGGTCC ATTGCTGGCC CCCGGCGACA AACCCATGAT	420
TGTAGTGCAG TACAAAGGCG AAAGAANAAG CAATTCCTCT GCCCGAAAGA AATCTCCTCC	480
CATGGTCCTC CATCAAGATG CCGCCGAAAT TGCCGAAAGC TTACCTCCGG AAACCCACCC	540
ATCAAGAAAT GCGGTGGTGA CGGTCCCTGC CTAATTCTAC GACTCCCAGC GGCANGCCCC	600
AAAGGATGCC CGAATTCATT GCGGGGCTCC AATGTTCTTG CNGATNCNTC NAATGAACCC	660
CACCTGGCTGC TGCCATTGCC TTNTGGTCCT TGGAAAAAA AGGCTTCAAC TT	712

## (2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 729 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: D-88

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

ACGAGATTCC CCCATCCCAT CAGATCTCGC TTCGGCTGAG CTCCCAGAAC CCTAATAATG	60
GTGCAGGAGG AGACTGACGC GCGGGCGGCT GATGAGCCCG TCGCTGATGC GGCCCCCTCT	120
GATCCGGTGG CGGAGGAGGA CCCCGTGGCT GCCGCTGACG CTGCCGCTGC CGCTGCTGCT	180
GATGCTAAGC CATCCAAGGG GAAGAAGGCG AAGGGCCCCA GTAAGGCCAA GGCCAAGGCC	240
AAGAAGCCTG CTACTCCACG GAAGCCGTCT GCCCACCCGC CGTACGCCGA GATGATCATG	300
GAGGCGATCG TGACGCTGAA GGAGCGCACC GGGTCGAGCC AGTATGCGAT CGGGAAGTTC	360
CTCGAGGACA AGCACAAGAA ATCACCCTCCC GGGAAACTTT CCGGAAGATC CTCCTCGGCC	420
AGCTGAAGAN GCTCACTGCT GCCGGTAAGC TCAAGAAAGG TTAAAGAACT CCTACAAGGT	480
AGCCGCCCGC CACCCGCCAC CTCCTCTTCC TCCGTCTCTC NGCTGCTCCG ACGAAACCTN	540
AACCGAAACC CAAGGCAGCC CACCAAGAAA ACCCGCTGCT TCCGACGAAA NACAAACCCC	600
AAGGGGAAAG GCCCCGCTG CCGCGAAACC CCAAGCCNNA AACTNAGCCG ATCCCCNGCN	660
GCCAAGCCCA ANGCCCAAAG CGAAACCCNG GNTCCCCCNG NCCNAACNGG AAAGCCAACC	720
NACCCGCNT	729

## (2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 750 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: D-141

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

ACGAGCGAGT TTTTTTTTTT TTTTTTATC ACCTTATTTG TCACTTTTCA TGCTATTCCT	60
GAGCATAGAT AATGGATGAT GCATGCTTAT TGATCTTGAT CGTTAGGACT TGATCATTGT	120
GCAAAAGCGG AGGAGGAGGA CTGTTGCAGA ACAAAGAGAA ACTACCCTGA AAGCTTTCCT	180
AGAGAGAGAA ACAAGACCAT CACACAGACA GACAGGGAAT GGTGGCATCA CCACATAATT	240
TACATAACCA GCAACTCCGT GGCTTTTGTA GTTCTACAG CAGTGGTCGT TTGCCCCATC	300
GCTTCCCTCT CTCTTTATTG TGTGCGCG ACAACCGCAG ACCCTTCCAC CTTGAAAGTG	360
GCACCACATA CTTCTTCCTC GTTTTCAAGA ACGGCGGTGA CCTTGTGCTT AGGATTCTCG	420
TAGCTTTTCA GGCCCCCAA TGCAATTGAA TTNGTAACAT CCTTTGGGGA ATGGTGCAAG	480
TTGACTTCCC CGCATGATCC CTTCAGCAAA TCCAGGTTCA TCAGCAAAGG CAAGGCATCC	540
ATCGGCTGTT ATGCCCCAGA AACAGGGTT ACCTTCCATC TGGGTCCGAT GCCAACAAAG	600
ANTGGATGAA ATTTGACTTG TCCAAANAAG ACAAAGGGGA AATTTGCCNG AAAAAATNT	660
NCCGAACCTT NAACTGGGC NGAATAAGGG GNTCCGGTCC CCCGAAGGCC TTTATNCNCC	720
TCCCATCACC ANCACCACCT CNTTTGGNGC	750

## (2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 729 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: D-60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

ACGAGATGTG GATCACTCTG ACCATTTGAA ATATGAAGAA CAAGCTAATT CTGGTGATGT	60
TGATATCAAA TCCTCTAAAG AAACAATAGA GTCTCCCTGT GAGCCACAGA TGAACCTCCT	120
GCATTCAACA TCATCTGCTA TGATGGTAGA TGTAGGGAAG GAGGATAAGT TTGCTAACCA	180
TGTGAGTCAA GAGGAGGAAC ACGAGAAACA AATTAAGTCA TCTTCGCCTA CTGCATCTCA	240
GCAAAATCAA TTCTCTCAGC TTGATGGTTC TAGACAAACT CAGGCTAGCC TGTTTATGGA	300
GATGCCACCT CAGAGTGAAG AAATGGAGGC AATCGATCAA TTGAAACAAG TCACTGCCAA	360
TTTACCTCCC AAAAGTTGAA AGCTCAATCA TTCCATGGAG ATGGAAGATG TTGATGACAA	420
AGTTGATTCC AGTTAATTGA TTTGGAAAGA CGAATTCCTC CCAATTGAAA GTTGAATCCC	480
TGTAATCCCT TCCGAAGGCC CAAGTTAAGT TTTTTTCCA TATAGCTGGT CCAATTTGTG	540
GAATGTTTTG ATATTTCTTA TGCCCATTTT TTCCTTGAAT TTATTANACC TTAATNTTTG	600
TACTCCCNCC CCCCACTANA ATGANTTTAT CCCTGAATGT TGGGTNATAA ANCCNGGAAC	660
NAAATTGAAT TTTCCCGGT TAAAAAGGT TTTTGAACCC CCCNGCCCA TTCCNAATNA	720

CCTCCCNCGG

729

## (2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 748 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: D-92

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CACGAGCCTC TCCGTATATC CTTGACTTCC CGGCTGCCTA AGAAGAGTTC TTCCGCGACT	60
TCCGTCACCG AAGGCCGAG TGGCGTTTGG ATTGAAGACG TTCTCTTCCC TCCACCATCT	120
CAGGCGGGGG GCCGTCGTGC CACCGGTTTT TCTTCGATTT TTTTGTAAAG TACTCAAATC	180
AAGGCCGATT GCGGTGACCG CTTACACGAT GGATCCGATT GAAGATCAAN ATCTGGAGAG	240
GAAACTAAAA AAGGAGCAAA AGGCTAAACT GAAAGAAGAG AAAAACTTA AGGCTGCACA	300
AAAGGCAGAA GCTGCAAAAC TCCAGGCACA AAGGTCATCT GATGGATCTA AGAAGAGTGA	360
GCGAAAACAG AGGAAAAGAG ATGTTGAAGA AGAGAATCCC GAGGATTTTA TGGACCCTCT	420
TACCCCGGTT GGGAGANAAA AAGCAGCTCT CTCGTCAAAT GGCCAAGCAA TATAATCCCA	480
GTGCTGTTGA AAAATCATGG TATTCATGGT GGAAGCATC AGATTTCTTT TACAGCAGAT	540
GCNAGCAGCT CAAAACCATC TTTTGTATT GTACTTCCAC CTCAAATGT TACTGGTGCT	600
CTTCCTATAG GTCATGGGCC TTAGTGCTGC TTTACAGGAC NCAATTNTCC GTTNGGAAAA	660
AAATTTCGGG CTACNATGTT CTATGGGTCC TGAATGGAC CATGCTGGCN TNNCANCCCA	720
GGTGGTCCTG GAAAAAATT TATGCCNG	748

## (2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 780 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: D-110

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

ACNAGCAAAA TCTTTGTTTT GCTTGGGTCG GGCCTTGCTC TCGGATCCTC TCCTGTTTCC	60
ACTGTTGCGG TTCCAATACG TCTCTCTTTC CCCTTTTTAT TTGTTTATTT TTACCTTTAT	120
TTATTCGTTT ATTTTTTG TGTTTTAGCT TGTGGGTTGT TCGGACCGGC GGCATCGTCA	180
CTTTTAGCGA TTTCTTGC GTTAGGAGTCTT CTTTCAAAAC CGACAGTAGT TTGTCCGGAT	240

TGGAGGGATG AAGGGGAAAG GAGCAACAGC TAAAACTAC TTTGTCCTCA ATACCGGAGC	300
CAAGATTCCT GCTGTTGGTC TTGCAACATG GCAACACGGA GGTGATCTTT GTGCTGAAGC	360
CGTGGCGACG GCCTTGACGG CCGGGTATCG CCACATCCGA CTGCACCCAT CCTATATGGG	420
AATGANGTTG ANGTTGGGAA AGGCGCTAGC CCGANGCTTT TGAAAGCGGA ACCAAGAAGG	480
AAAGATTTGT TCTTGACCTC CNAATTTGTA TTGTGCTACT AATTCCACAT AAGAAGGTCC	540
AANAATTCCC GTTGAAAATT TCCTTGAAAA ACCTTGCGCT CTCCTACTTG GATCTTGAT	600
CTTGTTCAC TGGCCTGAAT TGTTCCGCTC CCNGGGAATG CCACTGATCC TTCCTTGGGA	660
AATCTGCCA ACCAAATATA AACAGTCTCC NCNACAATGA ACCNACCTGG GAAGCTATGG	720
AAATCTTGTT CCGAAGGGCT TGTCTGCAA TGGTGTTTAC AATTCACATC NCAATCNCCA	780

## (2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 783 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: D-123

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

ACNAGCACAC TACGGAGGAG CATCCCGTGT GCCCGTCTCT TCTCTCTCTC	60
TCTCTCTCTC TCTCTCTCTC TGTCTCTGTT TCTCTCTCTG GTTCGGCCAT GGTGAAGGTC	120
ATGGCAACGG CAATGGCGTT GGTGTTGGCG TTCCTTCTCG CCGCCGGCGT AGGGCTGTCTG	180
GAGGGTGCTG TCTACAAGGT TGGGGATGCC ACCGGATGGA CCATCATGGG GAGCCCGAAC	240
TACACCGCCT GGGCGTTTTT CAAGAAATTC CAAGTGGGAG ACACCGTTGT GTTTGAGTAC	300
AACAAAAGCT TCCACAACGT GCTTGAGGTG AGCAAGGCCG ACTACCACTC CTGCAATGCA	360
GCATCGCCCA TGGCCACATT TGCCACCGGT AATGACACCA TCACGATCAA GACCAAGGGC	420
CACCGCTACT TCATCTGTGG CATCCCTGGA CACTGCAGCG GTGGCCAGAA NGTGGACATC	480
AAGATCTCCA AGTCTACCTC CTCTGCTGCC CTTCCACCT CGCCCACCGC CTCTCCTTCC	540
CCCTCCCCTG CTGCCTCCAC TCCCGGTGGT GGGTCNTGGA AGCATCTCCA CTCCGGCAGC	600
TGGCCTGGAN CTAACAGCNG GCACAAGAAC TCCTCCAAGA NTGAATGCTC TTGCTCCTTC	660
TTGTGTTTTG CATCTTGCTG CTGTCTCCNA ATTGGCCTTT GCCATAATTA TTAATCCCTG	720
ANAAATGTGA AAAAATAATA ANANTTGAAT TANTTTGGTT TTNAACCTNT GCAGAATTGT	780
TCT	783



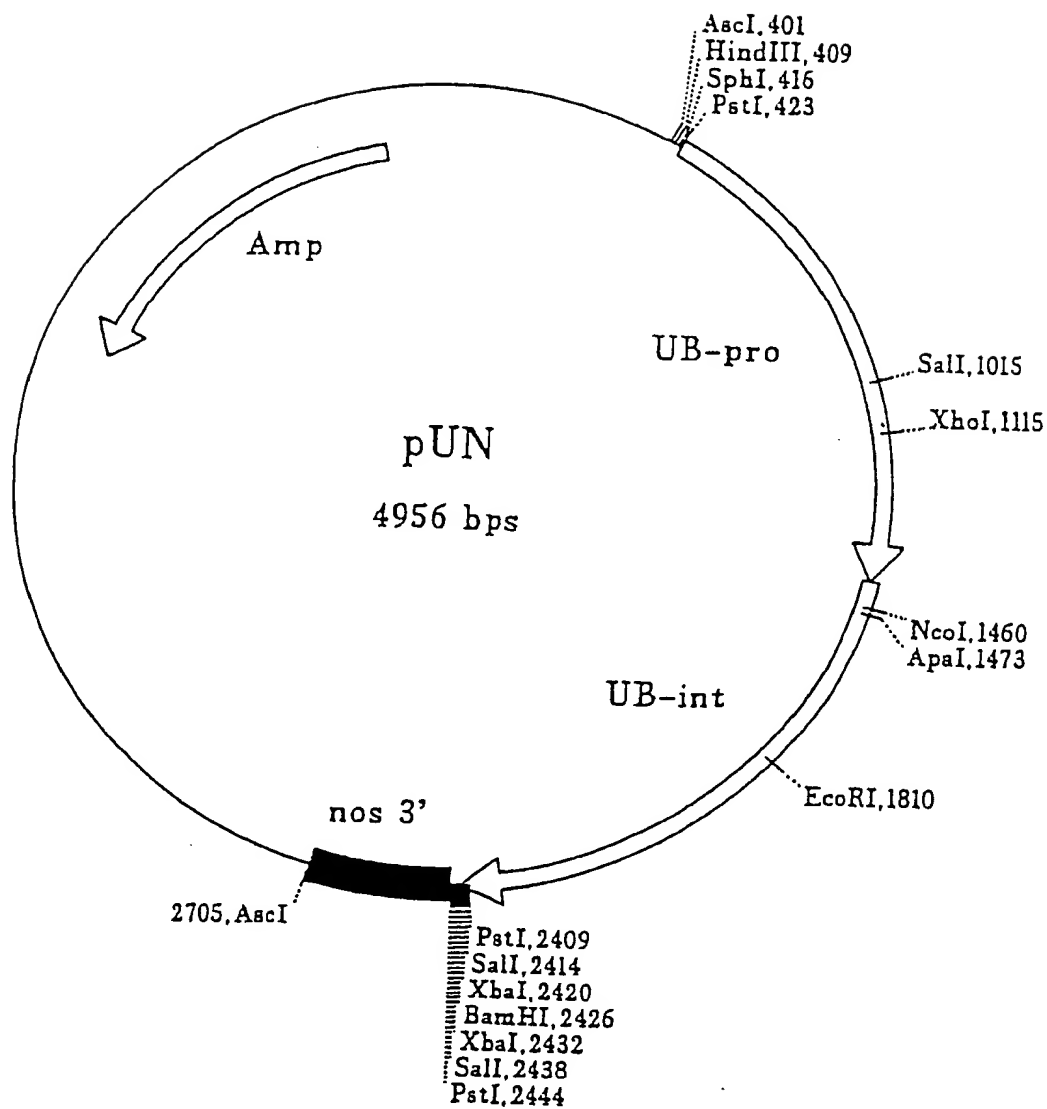
## CLAIMS

1. A method of modulating the fruit ripening or tissue senescence characteristics of a plant of the genus *Musa* comprising inserting into the genome of said plant a DNA construct comprising in sequence a promoter region which is operable in plant cells, a DNA insert having a nucleotide sequence selected from SEQ ID Nos. 1-73, complementary sequences of SEQ ID Nos. 1-73 and variants of said sequences permitted by degeneracy of the genetic code and a transcription termination sequence, and selecting from the population of regenerants those transformants with modulated fruit ripening or tissue senescence characteristics.
2. A method according to claim 1 wherein the said DNA insert comprises a full length polynucleotide coding sequence which includes a polynucleotide sequence as shown in any one of SEQ ID Nos. 1-73.
3. A method according to claim 1 or claim 2 wherein the said DNA construct comprises a promoter which is constitutive, developmentally regulated, or switchable.
4. A method according to claim 3 wherein said promoter is tissue specific or organ specific.
5. A method according to any one of claims 1 to 4 wherein the promoter is either the SAG 1 promoter, the polyubiquitin promoter or the banana ACC oxidase promoter.
6. A method according to any one of claims 1 to 5 wherein plants are transformed using the *Agrobacterium*, microparticle bombardment, fibre mediated or direct insertion method.

7. Plant material, plants, their progeny and seed produced according to a method as claimed in any one of claims 1 to 6, characterised in that said plant material and plants exhibit modulated ripening or tissue senescence characteristics.

1/3

FIGURE 1



2/3

FIGURE 2

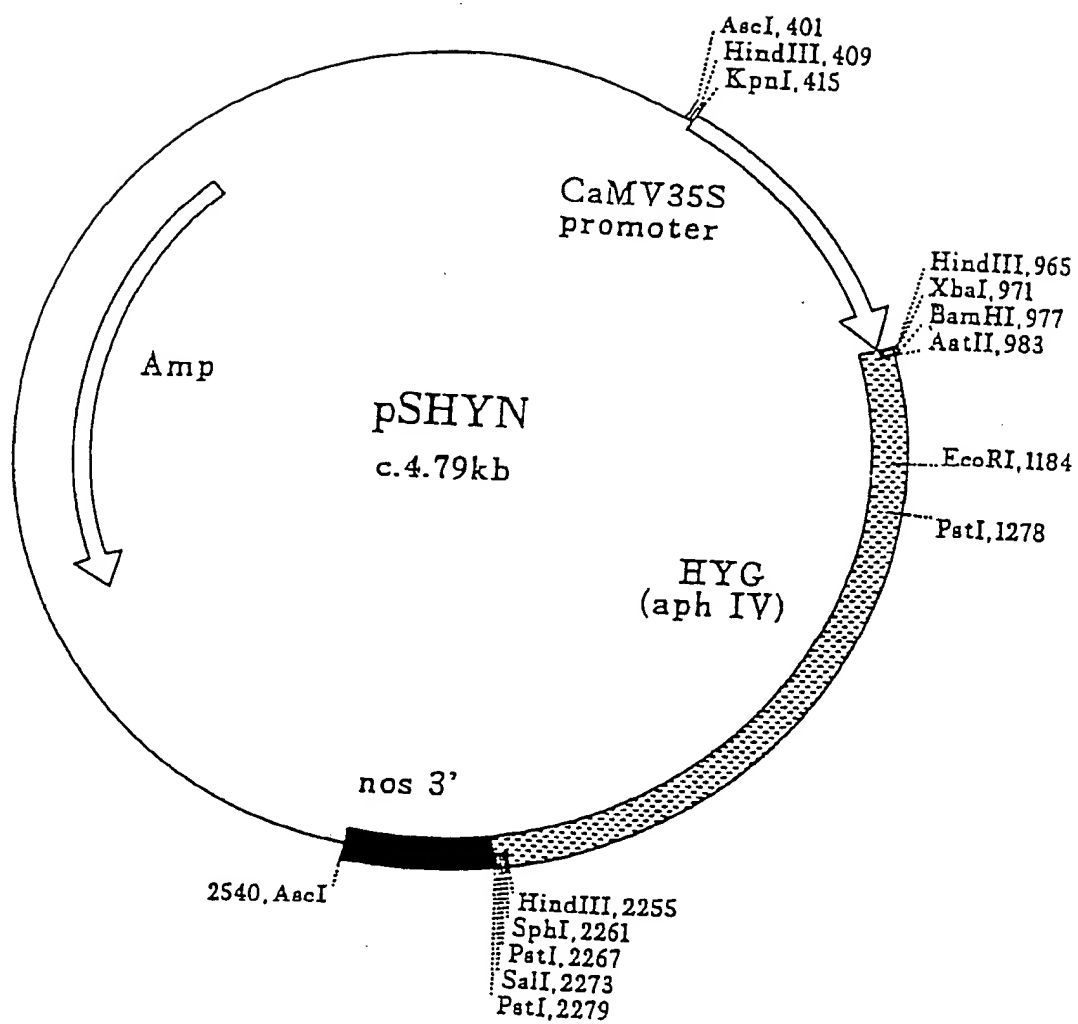
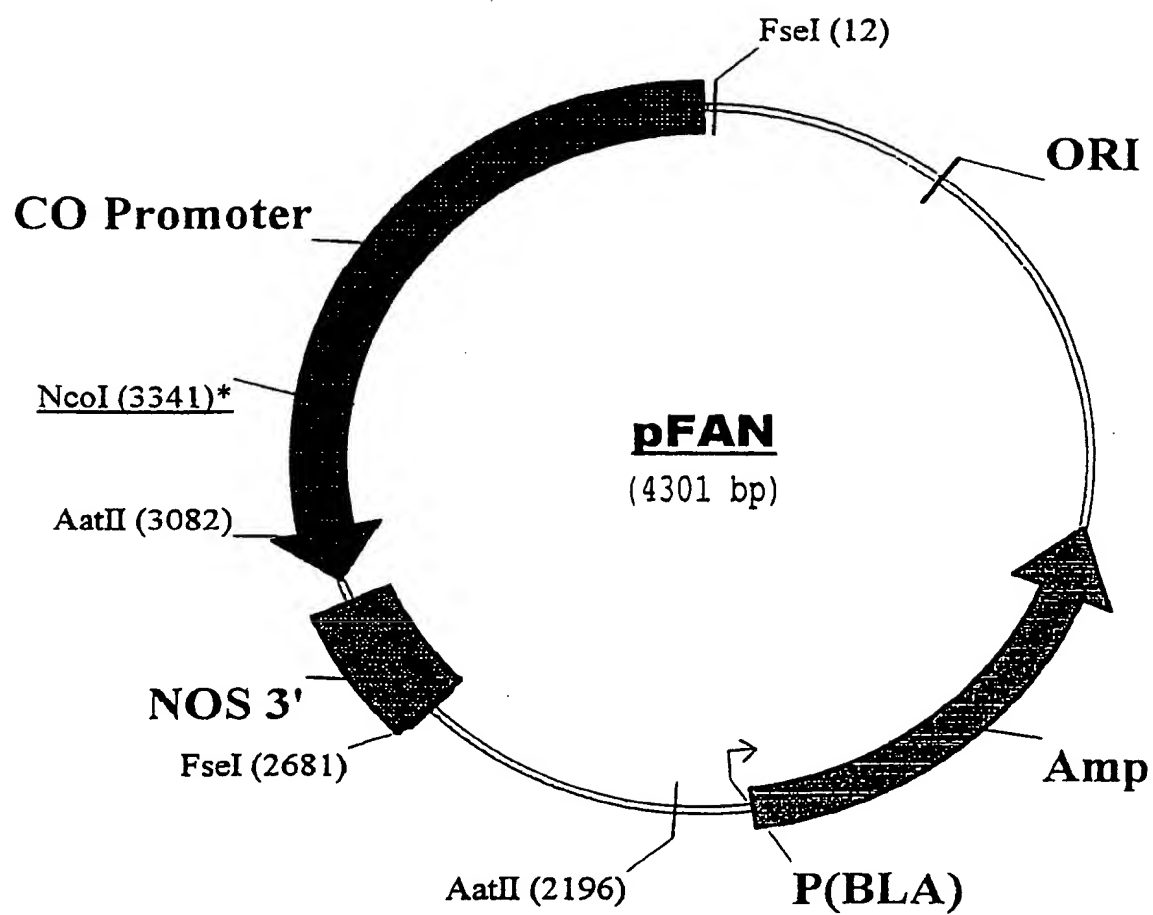


FIGURE 3



## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/82 C12N9/02 C12N15/29 C12Q1/68 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C12Q A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
------------	------------------------------------------------------------------------------------	-----------------------

X	HUANG P -L ET AL: "CHARACTERIZATION AND EXPRESSION ANALYSIS OF A BANANA GENE ENCODING 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE" BIOCHEMISTRY AND MOLECULAR BIOLOGY INTERNATIONAL, vol. 41, no. 5, April 1997, pages 941-950, XP000675954 especially page 942, line 9-14 see the whole document --- -/--	1-4,6,7
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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents :

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \* & \* document member of the same patent family

Date of the actual completion of the international search

4 August 1998

Date of mailing of the international search report

28.10.98

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Authorized officer

Holtorf, S

## INTERNATIONAL SEARCH REPORT

Intern Application No

PCT/GB 98/01297

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	LOPEZ-GOMEZ R ET AL: "ETHYLENE BIOSYNTHESIS IN BANANA FRUIT: ISOLATION OF A GENOMIC CLONE TO ACC OXIDASE AND EXPRESSION STUDIES" PLANT SCIENCE, vol. 123, no. 1/02, 1997, pages 123-131, XP000676021 see especially page 129, line 40-44 ---	1-7
A	MEDINA-SUAREZ R ET AL: "GENE EXPRESSION IN BANANA PEEL AND PULP DURING RIPENING" PLANT PHYSIOLOGY, vol. 111, no. 2, June 1996, page 122 XP002049412 see the whole document ---	1-7
A	CLENDENNEN S K ET AL: "ISOLATION AND IDENTIFICATION OF GENES DIFFERENTIALLY EXPRESSED DURING BANANA FRUIT RIPENING" PLANT PHYSIOLOGY, vol. 111, no. 2, June 1996, page 34 XP002049413 see the whole document ---	1-7
A	DOMINGUEZ-PUIGJANER E ET AL: "DIFFERENTIAL PROTEIN ACCUMULATION IN BANANA FRUIT DURING RIPENING" PLANT PHYSIOLOGY, vol. 98, no. 1, January 1992, pages 157-162, XP002049414 abstract, page 161, Fig.2 ---	1-7
A	WO 91 01375 A (ICI PLC) 7 February 1991 page 3, line 10; page 10 ---	1-7
A	WO 92 12249 A (MONSANTO CO) 23 July 1992 PAGES 3,4,7,14,21,25 ---	1-7
A	WO 95 15678 A (TEXAS A & M UNIVERSITY SYST ;ARNTZEN CHARLES J (US); MAY GREGORY D) 15 June 1995 PAGE 5 AND PAGE 14, LINE 1 ---	1-7
A	SAGI, L., ET AL.: "GENETIC TRANSFORMATION OF BANANA AND PLANTAIN (Musa spp.) VIA PARTICLE BOMBARDMENT" BIOTECHNOLOGY, vol. 13, May 1995, pages 481-485, XP002073183 cited in the application see the whole document ---	1-7
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# INTERNATIONAL SEARCH REPORT

Inter: nat Application No

PCT/GB 98/01297

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SEYMOUR G B: "BANANA" BIOCHEMISTRY OF FRUIT RIPENING, 1993, pages 83-106, XP002049415 see page 85 - page 86 ---	1-7
P,X	MEDINA-SUAREZ R ET AL: "GENE EXPRESSION IN THE PULP OF RIPENING BANANAS1 TWO-DIMENSIONAL SODIUM DODECYL SULFATE-POLYACRYLAMIDE GEL ELECTROPHORESIS OF IN VITRO TRANSLATION PRODUCTS AND CDNA CLONING OF 25 DIFFERENT RIPENING-RELATED MRNAS" PLANT PHYSIOLOGY, vol. 115, no. 2, October 1997, pages 453-461, XP002049416 see the whole document -----	1-6



# INTERNATIONAL SEARCH REPORT

Int. l. application No.

PCT/GB 98/ 01297

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheets

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet, subject 1.

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-7 partially

A method for modulating fruit ripening and senescence by generating transgenic banana plants using Aminocyclopropane carboxylic (ACC) oxidase - specific nucleotide sequences, namely SEQIDs 1-4, and complementary sequences thereto.

2. Claims: 1-7 partially

idem as subject 1, by using nucleotide sequences homologous to an Aconitase, namely SEQID No.5.

3. Claims: 1-7 partially

idem as subject 1, by using nucleotide sequences homologous to a Pectate Lyase I, namely SEQID No. 7,8,11,18,19 and 21.

4. Claims: 1-7 partially

idem as subject 1, by using nucleotide sequences homologous to a Pectate Lyase II, namely SEQID No.6,9,10,12-17 and 20.

5. Claims: 1-7 partially

idem as subject 1, by using nucleotide sequences homologous to an Endochitinase, namely SEQID No.22-27.

6. Claims: 1-7 partially

idem as subject 1, by using nucleotide sequences homologous to a Beta-1,3-Glucanase or Beta-(1,3:1,4)-D- Glucanase or Endo-1,3-beta-glucanase, namely SEQID No.28-39.

7. Claims: 1-7 partially

idem as subject 1, by using nucleotide sequences homologous to a Beta-glucosidase, namely SEQID No.40 and 41.

8. Claims: 1-7 partially

idem as subject 1, by using nucleotide sequences homologous to an UDP-glucose-pyrophosphorylase, namely SEQID No.42.

9. Claims: 1-7 partially